



#4

# Sequence Listing

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Botstein, David  
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Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.

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tatgcttctt ttggtcaaga aagctcaagg gagagttatt aatgtctcca 600  
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gccagcagt ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050  
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gcccattcaa aatgatctt accgtggcct gcccattgct tatggtcccc 1400  
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aaaaaaaa 1508

<210> 10  
<211> 319  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-17  
<223> Signal Peptide

<220>  
<221> misc\_feature  
<222> 36-47, 108-113, 166-171, 198-203, 207-212  
<223> N-myristoylation Sites.

<220>  
<221> misc\_feature  
<222> 39-42  
<223> Glycosaminoglycan Attachment Site.

<220>  
<221> TRANSMEM  
<222> 136-152  
<223> Transmembrane Domain

<220>  
<221> misc\_feature  
<222> 161-163, 187-190 and 253-256  
<223> N-glycosylation Sites.

<400> 10  
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1 5 10 15  
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys  
20 25 30  
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
35 40 45  
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
50 55 60  
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
65 70 75  
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
80 85 90  
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
95 100 105  
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
110 115 120

Pro Thr Asp Trp	Leu Thr Leu Glu Asp	Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe	Gly Leu Ile Ser Val	Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys	Ala Gln Gly Arg Val	Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu	Ala Ile Val Gly Gly	Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu	Gly Phe Asn Asp Ser	Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn	305	310	315
Pro Lys Ala Val					

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

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 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

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caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300  
gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
gggttaaaac cagcaaacc acccgcttta ccagctctc agaaggcgga 450  
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acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
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gagcgggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
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gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900  
cgcgctggac accatgtgga tcttgggtct gaggaaagaa tttgaggaag 950  
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000  
aacctgtttg agagcacgat ccgcatectg ggggggctcc tgagtgccta 1050  
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cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
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 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
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 aacctgctca goctggagc ctacgtgttc aacaccgaag cccaccctct 2100  
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 ggtgaccgag tggacagccc aggggtgcagc tctgcccggt ctctgaagc 2500  
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 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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Gln Ser Asp Phe	Leu Thr Pro Pro Val	Gly Gly Ala Pro Trp	Ala
	20	25	30
Val Ala Thr Thr	Val Val Met Tyr Pro	Pro Pro Pro Pro Pro	Pro
	35	40	45
His Arg Asp Phe	Ile Ser Val Thr Leu	Ser Phe Gly Glu Ser Tyr	
	50	55	60
Asp Asn Ser Lys	Ser Trp Arg Arg Arg	Ser Cys Trp Arg Lys Trp	
	65	70	75
Lys Gln Leu Ser	Arg Leu Gln Arg Asn Met	Ile Leu Phe Leu Leu	
	80	85	90
Ala Phe Leu Leu	Phe Cys Gly Leu Leu	Phe Tyr Ile Asn Leu Ala	
	95	100	105
Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	
	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	
	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	
	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	
	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	
	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	
	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	
	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	
	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	
	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	
	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	
	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	
	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	

	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val	Ser
	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe	Glu
	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His	Leu
	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly	Asn
	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr	Ser
	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp	Thr
	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu	Phe
	395	400	405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu	Ala
	410	415	420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys
	425	430	435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe
	440	445	450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr
	455	460	465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu
	470	475	480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg
	485	490	495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe	Val
	500	505	510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu
	515	520	525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly
	530	535	540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr
	545	550	555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu
	560	565	570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val

575										580					585				
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr					
				590					595					600					
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys					
				605					610					615					
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe					
				620					625					630					
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln					
				635					640					645					
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe					
				650					655					660					
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp					
				665					670					675					
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala					
				680					685					690					
His	Pro	Leu	Pro	Ile	Trp	Thr	Pro	Ala											
				695															

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

cgccagaagg gcgtgattga cgtc 24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

ccatccttct tcccagacag gccg 24

<210> 15

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcgccct 150  
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250  
cgggcagtcg ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300  
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
cccaccgcct ggcagtgtct gtgcccttcc gcgaacgctt cgaggagctc 400  
ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450  
gcaccacatc tacgtgtctc accaggtgga ccacttcagg ttcaaccggg 500  
cagcgctcat caacgtgggc ttccctggaga gcagcaacag cacggactac 550  
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tggttttctt gaggtgaggc ccttccacgt ggctccccg gagctccacc 650  
ctctctacca ctacaagacc tatgtcggcg gcactctgct gctctccaag 700  
cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750  
ccgcgaggac gacgagttct accggcgcct taaggagct gggctccagc 800  
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cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300  
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 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450  
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 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17  
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp  
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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
                   20                  25                  30  
  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
                   35                  40                  45

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala				50	55	60
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys				65	70	75
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp				80	85	90
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe				95	100	105
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser				110	115	120
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp				125	130	135
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu				140	145	150
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp				155	160	165
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala				170	175	180
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His				185	190	195
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His				200	205	210
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly				215	220	225
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu				230	235	240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe				245	250	255
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg				260	265	270
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly				275	280	285
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu				290	295	300
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp				305	310	315
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser							320	325	

<210> 18  
<211> 23  
<212> DNA  
<<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 18  
gcgaacgctt cgaggagtcc tgg 23

<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgtttgc ctatccacct cccccaagcc cctttacctg tgctgctgct 50  
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactgggtcgg tgcccagaaa gtctctttctg ccaactgaagc ccccatcagg 150  
gattggggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag ccagccccg tggggaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagatagggg acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gcctgttca ttaagaaatt gttcccttcc 400  
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450



taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18  
<223> Growth factor and cytokines receptors family.

<400> 22  
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1 5 10 15  
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30  
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45  
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
50 55 60  
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
65 70

<210> 23  
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<223> Signal peptide.

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<223> Transmembrane domain (type II).

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				110					115					120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
				125					130					135	
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Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	
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				185					190					195	
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Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	
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Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln	
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				365					370					375	
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro	
				380					385					390	
Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe	
				395					400					405	
Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val	
				410					415					420	
Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr	
				425					430					435	
Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu	
				440					445					450	
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu	
				455					460					465	
Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys	
				470					475					480	
Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu	
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Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala	
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Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg	
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Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile	
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Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met	
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Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly	
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<223> Synthetic oligonucleotide probe

<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

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 35 40 45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
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<211> 322  
<212> PRT  
<213> Homo sapiens

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35 40 45  
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
50 55 60  
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
65 70 75  
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
80 85 90  
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
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Ala Cys Tyr Ala	Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr	
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Pro Thr Thr Tyr	Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp	
125	130	135
His Ala Ile Ala	Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala	
140	145	150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile	
155	160	165
Thr Gly Tyr Met	Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu	
170	175	180
Thr Phe Val Ala	Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn	
185	190	195
Leu Tyr Gln His	Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr	
200	205	210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu	
215	220	225
Gly Glu Cys Thr	Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu	
230	235	240
Ser Gly Leu Ala	Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu	
245	250	255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln	
260	265	270
Pro Arg Arg Ser	Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr	
275	280	285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr	
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 <212> DNA  
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<210> 33  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 33  
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 Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val  
 35 40 45  
 His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu  
 50 55 60  
 Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu  
 65 70 75  
 Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro  
 80 85 90  
 Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys  
 95 100 105  
 Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala  
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Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg	125	130	135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys	140	145	150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp	155	160	165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala	170	175	180
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly	185	190	195
His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu	200	205	210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser	215	220	225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu	230	235	240
Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro	245	250	255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala	260	265	270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser	275	280	285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu	290	295	300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser	305	310	315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala	320	325	330
Glu	Pro	Glu	Glu	Gln											335		

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

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<210> 35  
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<220>  
<223> Synthetic oligonucleotide probe

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<210> 36  
<211> 25  
<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 37  
<211> 23  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 37  
ggcgagccct aactatccag gag 23

<210> 38  
<211> 39  
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<220>  
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<400> 38  
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<210> 39  
<211> 22  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 39  
ctgctgcaaa gcgagcctct tg 22

<210> 40  
<211> 2084

<212> DNA  
<213> Homo sapiens

<400> 40

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<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

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Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn
				20					25					30
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
				35					40					45
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
				50					55					60
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
				65					70					75
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
				80					85					90
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
				95					100					105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val	110	115	120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser	125	130	135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr	140	145	150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser	155	160	165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val	170	175	180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser	185	190	195
Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu	200	205	210
Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn	215	220	225
Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe	230	235	240
Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu	245	250	255
Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser	260	265	270
His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu	275	280	285
Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser	290	295	300
Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu	305	310	315
Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu	320	325	330

Arg Thr Ser Val

<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

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tgtgtagggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550

ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20						25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35						40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
			50						55					60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65						70					75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80						85					90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95						100					105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110						115					120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125						130					135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140						145					150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155						160					165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170						175					180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185						190					195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200						205					210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215						220					225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

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	245	250	255
Val Glu Thr Lys Ile Cys Gln Glu			
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<210> 44  
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 <212> DNA  
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 <223> Synthetic oligonucleotide probe

<400> 44  
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<210> 45  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 45  
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<210> 46  
 <211> 26  
 <212> DNA  
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<400> 46  
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<210> 47  
 <211> 28  
 <212> DNA  
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<220>  
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<400> 47  
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<210> 48  
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 <212> DNA  
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<220>

<223> Synthetic oligonucleotide probe

<400> 48

cacgattccc tccacagcaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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 aaaaaaaaa aaaaaaaga 1969

<210> 50  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
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 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
 35 40 45  
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
 50 55 60  
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
 65 70 75  
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

80										85				90			
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala			
				95					100					105			
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln			
				110					115					120			
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys			
				125					130					135			
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe			
				140					145					150			
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala			
				155					160					165			
Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr			
				170					175					180			
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp			
				185					190					195			
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys			
				200					205					210			
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro			
				215					220					225			
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu			
				230					235					240			
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly			
				245					250					255			
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro			
				260					265					270			
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val					
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 <211> 1734  
 <212> DNA  
 <213> Homo sapiens

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<211> 440  
<212> PRT  
<213> Homo sapiens

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Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
35 40 45  
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly  
50 55 60  
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr  
65 70 75  
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly  
80 85 90  
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala  
95 100 105  
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val  
110 115 120  
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val  
125 130 135  
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile  
140 145 150  
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro  
155 160 165  
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser  
170 175 180  
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln  
185 190 195  
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly  
200 205 210  
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln  
215 220 225  
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly  
230 235 240

Ser Ser Asn Ser	Gly Gly Gly Ser Gly	Ser Gln Ser Gly Ser Ser	245	250	255
Gly Ser Gly Ser	Asn Gly Asp Asn Asn	Asn Gly Ser Ser Ser Gly	260	265	270
Gly Ser Ser Ser	Gly Ser Ser Ser Gly	Ser Ser Ser Gly Gly Ser	275	280	285
Ser Gly Gly Ser	Ser Gly Gly Ser Ser	Gly Asn Ser Gly Gly Ser	290	295	300
Arg Gly Asp Ser	Gly Ser Glu Ser Ser	Trp Gly Ser Ser Thr Gly	305	310	315
Ser Ser Ser Gly	Asn His Gly Gly Ser	Gly Gly Gly Asn Gly His	320	325	330
Lys Pro Gly Cys	Glu Lys Pro Gly Asn	Glu Ala Arg Gly Ser Gly	335	340	345
Glu Ser Gly Ile	Gln Gly Phe Arg Gly	Gln Gly Val Ser Ser Asn	350	355	360
Met Arg Glu Ile	Ser Lys Glu Gly Asn	Arg Leu Leu Gly Gly Ser	365	370	375
Gly Asp Asn Tyr	Arg Gly Gln Gly Ser	Ser Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val	Gly Gly Val Asn Thr	Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe	Asn Phe Asp Thr Phe	Trp Lys Asn Phe Lys Ser	410	415	420
Lys Leu Gly Phe	Ile Asn Trp Asp Ala	Ile Asn Lys Asp Gln Arg	425	430	435
Ser Ser Arg Ile	Pro		440		

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 <211> 3580  
 <212> DNA  
 <213> Homo sapiens

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 <211> 280  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
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 Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu  
 35 40 45  
 His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr  
 50 55 60  
 Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser  
 65 70 75  
 Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys  
 80 85 90  
 Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln  
 95 100 105  
 Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His  
 110 115 120  
 Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu  
 125 130 135  
 Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val  
 140 145 150

Ala Asp Leu Val	Arg Gln Ala Glu Ser	Leu Leu Gln Glu Gln Leu
155	160	165
Val Thr Gln Gly	Glu Glu Gly Gly Asp	Pro Ala Gln Leu Leu Glu
170	175	180
Ile Leu Cys Ser	Gln Leu Cys Pro His	Gly Ala Gln Ala Leu Ala
185	190	195
Leu Gly Arg Glu	Phe Cys Gln Arg Lys	Ser Pro Gly Ala Val Arg
200	205	210
Ala Leu Leu Pro	Glu Glu Thr Pro Ala	Ala Val Leu Ser Ser Ala
215	220	225
Glu Asn Ile Ala	Val Gly Leu Ala Thr	Glu Lys Ala Cys Ala Trp
230	235	240
Leu Ser Ala Asn	Ile Thr Ala Leu Ile	Arg Arg Glu Val Lys Ala
245	250	255
Ala Val Ser Arg	Thr Leu Arg Ala Gln	Gly Pro Glu Pro Ala Ala
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Arg Gly Glu Arg	Arg Gly Cys Ser Arg	Ala
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 <211> 2401  
 <212> DNA  
 <213> Homo sapiens

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<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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				20					25					30
Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg
				35					40					45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro
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Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val
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Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro
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Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro
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Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg
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Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln
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Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly
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Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val
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Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala

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Glu	Thr	Gly	Lys	Asp 200	Arg	Glu	Lys	Ser	His 205	Ser	Trp	Leu	Ser	Thr 210
Gly	Trp	Phe	Thr	Met 215	Val	Ile	Ala	Val	Glu 220	Leu	Cys	Asp	His	Val 225
His	Val	Tyr	Gly	Met 230	Val	Pro	Pro	Asn	Tyr 235	Cys	Ser	Gln	Arg	Pro 240
Arg	Leu	Gln	Arg	Met 245	Pro	Tyr	His	Tyr	Tyr 250	Glu	Pro	Lys	Gly	Pro 255
Asp	Glu	Cys	Val	Thr 260	Tyr	Ile	Gln	Asn	Glu 265	His	Ser	Arg	Lys	Gly 270
Asn	His	His	Arg	Phe 275	Ile	Thr	Glu	Lys	Arg 280	Val	Phe	Ser	Ser	Trp 285
Ala	Gln	Leu	Tyr	Gly 290	Ile	Thr	Phe	Ser	His 295	Pro	Ser	Trp	Thr	

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caaaccatca tcgtcaccaa aggccagagt ctcatcttgg agtgtgtggc 1100  
cagtggaaatc ccacccccac gggtcacctg ggccaaggat gggtcacgtg 1150  
tcaccggcta caacaagacg cgcttcctgc tgagcaacct cctcatcgac 1200  
accaccagcg aggaggactc aggcacctac cgctgcatgg ccgacaatgg 1250  
ggttgggcag cccggggcag cggtcacact ctacaatgtc caggtgtttg 1300  
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cagagtgccca agcttacctg tgagggtcgt gggaaccccc cgccctccgt 1400  
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gtctaccagt gcatggccga gaacgaggtt gggagcgccc atgccgtagt 1550  
ccagctgcgg acctccaggc caagcataac cccaaggcta tggcaggatg 1600  
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accagacttg accccgggag ctgtgatgaa gtggagatgg cagcttacia 2000  
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tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100  
cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150  
aataggggct gcccctcggc tgcagtgggc taccgggca tgaagcccca 3200  
gcagcactgc ccaggcgagc ttcagcagca gagtgcacc agcagcctgc 3250  
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acgaggggtc ccaagtctag cccggacgag ggctctttct tatacacact 3350  
gcccagcagc tccactcacc agctgctgca gcccacac gactgctgcc 3400  
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 cctaacagga gtcacccagg aaagcaccgc acaggctggc gcgggacaga 3950  
 ctctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000  
 agataagctg gcaagaggaa ggatcccagg cacatgggtc atcacgagca 4050  
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 atggctggat ccggtgctac gggaaacatt ttcctaagat gcccatgaga 4150  
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200  
 caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250  
 aataaatggt tagtcttccc tgtaaaa 4277

<210> 58  
 <211> 1115  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro Glu  
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 Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala  
 20 25 30  
 Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr  
 35 40 45  
 Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu  
 50 55 60  
 Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu  
 65 70 75  
 Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr  
 80 85 90

Leu Val Ile Thr	Ala Leu Asn Asn His	Thr Val Gly Arg Tyr	Gln
95	100		105
Cys Val Ala Arg	Met Pro Ala Gly Ala	Val Ala Ser Val Pro	Ala
110	115		120
Thr Val Thr Leu	Ala Asn Leu Gln Asp	Phe Lys Leu Asp Val	Gln
125	130		135
His Val Ile Glu	Val Asp Glu Gly Asn	Thr Ala Val Ile Ala	Cys
140	145		150
His Leu Pro Glu	Ser His Pro Lys Ala	Gln Val Arg Tyr Ser	Val
155	160		165
Lys Gln Glu Trp	Leu Glu Ala Ser Arg	Gly Asn Tyr Leu Ile	Met
170	175		180
Pro Ser Gly Asn	Leu Gln Ile Val Asn	Ala Ser Gln Glu Asp	Glu
185	190		195
Gly Met Tyr Lys	Cys Ala Ala Tyr Asn	Pro Val Thr Gln Glu	Val
200	205		210
Lys Thr Ser Gly	Ser Ser Asp Arg Leu	Arg Val Arg Arg Ser	Thr
215	220		225
Ala Glu Ala Ala	Arg Ile Ile Tyr Pro	Pro Glu Ala Gln Thr	Ile
230	235		240
Ile Val Thr Lys	Gly Gln Ser Leu Ile	Leu Glu Cys Val Ala	Ser
245	250		255
Gly Ile Pro Pro	Pro Arg Val Thr Trp	Ala Lys Asp Gly Ser	Ser
260	265		270
Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu
275	280		285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met
290	295		300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu	Tyr
305	310		315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser
320	325		330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu
335	340		345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala
350	355		360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala
365	370		375

Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	380	385	390
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	395	400	405
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	410	415	420
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	425	430	435
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	440	445	450
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	455	460	465
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	470	475	480
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	485	490	495
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	500	505	510
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	515	520	525
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	530	535	540
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	545	550	555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg	560	565	570
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln	575	580	585
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp	590	595	600
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile	605	610	615
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg	620	625	630
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys	635	640	645
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly	
				665					670					675	
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu	
				680					685					690	
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr	
				695					700					705	
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr	
				710					715					720	
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met	
				725					730					735	
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr	
				740					745					750	
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys	
				755					760					765	
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His	
				770					775					780	
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn	
				785					790					795	
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr	
				800					805					810	
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro	
				815					820					825	
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	
				830					835					840	
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	
				845					850					855	
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	



Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu	950	955	960
Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His	965	970	975
Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly	980	985	990
Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro	995	1000	1005
Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys	1010	1015	1020
Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg	1025	1030	1035
Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro	1040	1045	1050
Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu	1055	1060	1065
Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp	1070	1075	1080
Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly	1085	1090	1095
Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr	1100	1105	1110
Pro Pro Leu Thr Ile	1115		

<210> 59  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 59  
 gggaaacaca gcagtcattg cctgc 25

<210> 60  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 60  
 gcacacgtag cctgtcgctg gagc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 61  
caccctaaag ccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
cgaggagctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccat 50  
cgctgtctcc tcccaggctc ccgcggccga ccccgcgca acatgcagcc 100  
cacgggcccgc gagggttccc gcgcgctcag ccggcggtat ctgcggcgtc 150  
tgctgtcctt gctactgtg ctgctgtgc ggcagcccgt aaccgcgcgcg 200  
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250  
cctcttcacc acgcgggtg tcccagcgc cctcactacc ccaggcctca 300  
ctacgccagg caccctaaa accctggacc ttgggggtcg cgcgcaggcc 350  
ctgatgcgga gtttccact cgtggacggc cacaatgacc tgccccaggt 400  
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500  
gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550  
cgtgcgcctc gccctggagc agattgacct cattcacgc atgtgtgcct 600  
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caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700  
cagcctctct gtgtgcgca gtttctatgt gctgggggtg cgctacctga 750  
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800  
agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850

agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900  
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 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000  
 tcccgatgat atcctgcagc ttctgaagaa cggtggcacg gtgatggtga 1050  
 cactgtccat ggggggtgctg cagtgaacc tgcttgctaa cgtgtccact 1100  
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150  
 cgggattggt ggaaattatg acgggactgg ccggttccct caggggctgg 1200  
 aggatgtgtc cacataccca gtcctgatag aggagttgct gagtctgasc 1250  
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 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350  
 tggaggctga gtttccatat gggcaactga gcacatcctg ccactcccac 1400  
 ctctgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450  
 gccaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500  
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550  
 tgctgacaca gtcgggtccc gcagaggtca ctgtggcaaa gcctcacaaa 1600  
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
 cacatggaaa a 1661

<210> 63  
 <211> 487  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63  
 Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg  
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 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg  
                     20                    25                    30  
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala  
                     35                    40                    45  
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val  
                     50                    55                    60

Pro	Ser	Ala	Leu	Thr 65	Thr	Pro	Gly	Leu	Thr 70	Thr	Pro	Gly	Thr	Pro 75
Lys	Thr	Leu	Asp	Leu 80	Arg	Gly	Arg	Ala	Gln 85	Ala	Leu	Met	Arg	Ser 90
Phe	Pro	Leu	Val	Asp 95	Gly	His	Asn	Asp	Leu 100	Pro	Gln	Val	Leu	Arg 105
Gln	Arg	Tyr	Lys	Asn 110	Val	Leu	Gln	Asp	Val 115	Asn	Leu	Arg	Asn	Phe 120
Ser	His	Gly	Gln	Thr 125	Ser	Leu	Asp	Arg	Leu 130	Arg	Asp	Gly	Leu	Val 135
Gly	Ala	Gln	Phe	Trp 140	Ser	Ala	Ser	Val	Ser 145	Cys	Gln	Ser	Gln	Asp 150
Gln	Thr	Ala	Val	Arg 155	Leu	Ala	Leu	Glu	Gln 160	Ile	Asp	Leu	Ile	His 165
Arg	Met	Cys	Ala	Ser 170	Tyr	Ser	Glu	Leu	Glu 175	Leu	Val	Thr	Ser	Ala 180
Glu	Gly	Leu	Asn	Ser 185	Ser	Gln	Lys	Leu	Ala 190	Cys	Leu	Ile	Gly	Val 195
Xaa	Gly	Gly	His	Ser 200	Leu	Asp	Ser	Ser	Leu 205	Ser	Val	Leu	Arg	Ser 210
Phe	Tyr	Val	Leu	Gly 215	Val	Arg	Tyr	Leu	Thr 220	Leu	Thr	Phe	Thr	Cys 225
Ser	Thr	Pro	Trp	Ala 230	Glu	Ser	Ser	Thr	Lys 235	Phe	Arg	His	His	Met 240
Tyr	Thr	Asn	Val	Ser 245	Gly	Leu	Thr	Ser	Phe 250	Gly	Glu	Lys	Val	Val 255
Glu	Glu	Leu	Asn	Arg 260	Leu	Gly	Met	Met	Ile 265	Asp	Leu	Ser	Tyr	Ala 270
Ser	Asp	Thr	Leu	Ile 275	Arg	Arg	Val	Leu	Glu 280	Val	Ser	Gln	Ala	Pro 285
Val	Ile	Phe	Ser	His 290	Ser	Ala	Ala	Arg	Ala 295	Val	Cys	Asp	Asn	Leu 300
Leu	Asn	Val	Pro	Asp 305	Asp	Ile	Leu	Gln	Leu 310	Leu	Lys	Asn	Gly	Gly 315
Ile	Val	Met	Val	Thr 320	Leu	Ser	Met	Gly	Val 325	Leu	Gln	Cys	Asn	Leu 330
Leu	Ala	Asn	Val	Ser 335	Thr	Val	Ala	Asp	His 340	Phe	Asp	His	Ile	Arg 345

Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp
350		355 360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr
365		370 375
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu
380		385 390
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg
395		400 405
Gln Val Glu Lys	Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val
410		415 420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser
425		430 435
His Leu Val Pro	Gln Asn Gly His Gln	Ala Thr His Leu Glu Val
440		445 450
Thr Lys Gln Pro	Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala
455		460 465
Ser Pro Tyr Leu	Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro
470		475 480
Thr Phe Thr Gln	Trp Leu Cys	
485		

<210> 64

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50  
aacaccacac gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100  
ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150  
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200  
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250  
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350  
agtgcaggta cgaggagcgc agcaccacca ccatcaaggc catcattgtc 400  
atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttctgat 450  
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
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 <211> 183  
 <212> PRT  
 <213> Homo sapiens

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 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
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 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
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 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
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 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
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 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
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Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
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<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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				20					25					30
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45
Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly
				50					55					60
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala
				65					70					75
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys
				80					85					90
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg
				95					100					105
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr
				110					115					120

Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
				125					130					135
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140					145					150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155					160					165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170					175					180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185					190					195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200					205					210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215					220					225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230					235					240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
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Cys Gln Lys Ile

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

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<210> 72  
 <211> 363  
 <212> PRT  
 <213> Homo sapiens

<400> 72

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				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
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Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
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Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

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Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn		
305	310	315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr		
320	325	330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg		
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Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp		
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Leu Ile Arg		

<210> 73  
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 <212> DNA  
 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

<400> 73  
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<210> 74  
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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 74  
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<210> 75  
 <211> 50  
 <212> DNA  
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<210> 76  
 <211> 1989  
 <212> DNA  
 <213> Homo sapiens

<400> 76

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<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
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50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75  
Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His  
80 85 90  
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His  
95 100 105  
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg  
110 115 120  
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro  
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Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150

cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

atctttcttca gcctgggcat tggcagtcta ctgcatgga acttctttat 250  
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ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350  
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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

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Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	
				20				25						30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	
				35				40						45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	
				50				55						60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	
				65				70						75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	
				80				85						90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	
				95				100						105	
Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	
				110				115						120	
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	
				125				130						135	

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr	140	145	150
Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe	155	160	165
Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr	170	175	180
Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met	185	190	195
Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr	200	205	210
Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp	215	220	225
Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe	230	235	240
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu	245	250	255
Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe	260	265	270
Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser	275	280	285
Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro	290	295	300
Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val	305	310	315
Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile	320	325	330
Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe	335	340	345
Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu	350	355	360
Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn	365	370	375
Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile	380	385	390
Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys	395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser	410	415	420

Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu
				425					430					435
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly
				440					445					450
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser
				455					460					465
Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile					
				470					475					

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 80  
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<210> 81  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 81  
 cgtaggtgac acagaagccc agg 23

<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 82  
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83  
 <211> 1844  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 tcctcgtcct cgtccccatc ctctcagcc tgggtggcctc ccaggactgg 150

aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200  
ctatgagcag ctgctcaagg tgggtgacctg ggggctcaat cggaccctga 250  
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cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165  
 Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
 170 175 180  
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
 185 190 195

Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His	Thr
200	205	210	
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro	Ala
215	220	225	
Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe	Tyr
230	235	240	
Leu Ser Phe Ala	Glu Ala Leu Arg Ala	His Ser Cys Leu Ser	Asp
245	250	255	
Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu	Pro
260	265	270	
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn	Ala
275	280	285	
Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val	Gln
290	295	300	
Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys	Ala
305	310	315	
Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg	Ile
320	325	330	
Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu	Arg
335	340	345	
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe	Arg
350	355	360	
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser	Asn
365	370	375	
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg	Glu
380	385	390	
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala	Ala
395	400	405	
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala	Leu
410	415	420	
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu	Trp
425	430	435	
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His	Ser
440	445	450	
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr	Glu
455	460	465	
Lys Asp Asp Trp	Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala	Gly
470	475	480	



Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
				545					550					555
Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
				560					565					

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20					25					30	

Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser

	35		40		45
Gln Gly Leu Asn Phe	Leu Leu Leu Phe	Thr Lys Met Leu Phe	Ile		
	50		55		60
Phe Asn Phe Leu Phe	Ser Pro Leu Pro	Thr Pro Ala Leu Ile	Cys		
	65		70		75
Ile Leu Thr Phe Gly	Ala Ala Ile Phe	Leu Trp Leu Ile Thr	Arg		
	80		85		90
Pro Gln Pro Val Leu	Pro Leu Leu Asp	Leu Asn Asn Gln Ser	Val		
	95		100		105
Gly Ile Glu Gly Gly	Ala Arg Lys Gly	Val Ser Gln Lys Asn	Asn		
	110		115		120
Asp Leu Thr Ser Cys	Cys Phe Ser Asp	Ala Lys Thr Met Tyr	Glu		
	125		130		135
Val Phe Gln Arg Gly	Leu Ala Val Ser	Asp Asn Gly Pro Cys	Leu		
	140		145		150
Gly Tyr Arg Lys Pro	Asn Gln Pro Tyr	Arg Trp Leu Ser Tyr	Lys		
	155		160		165
Gln Val Ser Asp Arg	Ala Glu Tyr Leu	Gly Ser Cys Leu Leu	His		
	170		175		180
Lys Gly Tyr Lys Ser	Ser Pro Asp Gln	Phe Val Gly Ile Phe	Ala		
	185		190		195
Gln Asn Arg Pro Glu	Trp Ile Ile Ser	Glu Leu Ala Cys Tyr	Thr		
	200		205		210
Tyr Ser Met Val Ala	Val Pro Leu Tyr	Asp Thr Leu Gly Pro	Glu		
	215		220		225
Ala Ile Val His Ile	Val Asn Lys Ala	Asp Ile Ala Met Val	Ile		
	230		235		240
Cys Asp Thr Pro Gln	Lys Ala Leu Val	Leu Ile Gly Asn Val	Glu		
	245		250		255
Lys Gly Phe Thr Pro	Ser Leu Lys Val	Ile Ile Leu Met Asp	Pro		
	260		265		270
Phe Asp Asp Asp Leu	Lys Gln Arg Gly	Glu Lys Ser Gly Ile	Glu		
	275		280		285
Ile Leu Ser Leu Tyr	Asp Ala Glu Asn	Leu Gly Lys Glu His	Phe		
	290		295		300
Arg Lys Pro Val Pro	Pro Ser Pro Glu	Asp Leu Ser Val Ile	Cys		
	305		310		315
Phe Thr Ser Gly Thr	Thr Gly Asp Pro	Lys Gly Ala Met Ile	Thr		

320					325					330				
His	Gln	Asn	Ile	Val	Ser	Asn	Ala	Ala	Ala	Phe	Leu	Lys	Cys	Val
				335					340					345
Glu	His	Ala	Tyr	Glu	Pro	Thr	Pro	Asp	Asp	Val	Ala	Ile	Ser	Tyr
				350					355					360
Leu	Pro	Leu	Ala	His	Met	Phe	Glu	Arg	Ile	Val	Gln	Ala	Val	Val
				365					370					375
Tyr	Ser	Cys	Gly	Ala	Arg	Val	Gly	Phe	Phe	Gln	Gly	Asp	Ile	Arg
				380					385					390
Leu	Leu	Ala	Asp	Asp	Met	Lys	Thr	Leu	Lys	Pro	Thr	Leu	Phe	Pro
				395					400					405
Ala	Val	Pro	Arg	Leu	Leu	Asn	Arg	Ile	Tyr	Asp	Lys	Val	Gln	Asn
				410					415					420
Glu	Ala	Lys	Thr	Pro	Leu	Lys	Lys	Phe	Leu	Leu	Lys	Leu	Ala	Val
				425					430					435
Ser	Ser	Lys	Phe	Lys	Glu	Leu	Gln	Lys	Gly	Ile	Ile	Arg	His	Asp
				440					445					450
Ser	Phe	Trp	Asp	Lys	Leu	Ile	Phe	Ala	Lys	Ile	Gln	Asp	Ser	Leu
				455					460					465
Gly	Gly	Arg	Val	Arg	Val	Ile	Val	Thr	Gly	Ala	Ala	Pro	Met	Ser
				470					475					480
Thr	Ser	Val	Met	Thr	Phe	Phe	Arg	Ala	Ala	Met	Gly	Cys	Gln	Val
				485					490					495
Tyr	Glu	Ala	Tyr	Gly	Gln	Thr	Glu	Cys	Thr	Gly	Gly	Cys	Thr	Phe
				500					505					510
Thr	Leu	Pro	Gly	Asp	Trp	Thr	Ser	Gly	His	Val	Gly	Val	Pro	Leu
				515					520					525
Ala	Cys	Asn	Tyr	Val	Lys	Leu	Glu	Asp	Val	Ala	Asp	Met	Asn	Tyr
				530					535					540
Phe	Thr	Val	Asn	Asn	Glu	Gly	Glu	Val	Cys	Ile	Lys	Gly	Thr	Asn
				545					550					555
Val	Phe	Lys	Gly	Tyr	Leu	Lys	Asp	Pro	Glu	Lys	Thr	Gln	Glu	Ala
				560					565					570
Leu	Asp	Ser	Asp	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Arg	Trp
				575					580					585
Leu	Pro	Asn	Gly	Thr	Leu	Lys	Ile	Ile	Asp	Arg	Lys	Lys	Asn	Ile
				590					595					600
Phe	Lys	Leu	Ala	Gln	Gly	Glu	Tyr	Ile	Ala	Pro	Glu	Lys	Ile	Glu

	605	610	615
Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His	620	625	630
Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp	635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly	650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile	665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr	680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser	695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly	710	715	720
Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu	725	730	735
His Ile Gln Asp			

<210> 87  
 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

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 ccaggacatt ggtgaccgc caatccggt tggacgactg gaagcccagc 150  
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200  
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250  
 caggggccgt gcttttctg ctggtgactg tcattgtcaa tatcaagttg 300  
 atcctggaca ctcggcgagc catcagtga gccaatgaag acccagagcc 350  
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400  
 gaggcagtgg tccccggcgg gtctggacg tagaggtgta ttcaagtcgc 450  
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500  
 ccgggagcag ggccggggca tccatgtcat tgtctcaac caggccacgg 550

gccacgtgat ggcaaaacgt gtgtttgaca cgtactcacc tcatgaggat 600  
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ctctgctgag gagcctgggc agccaggctg gccctgccct gggctggagg 750  
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acattctaag tcacctgccc tctcttcctg gggggacca gtctgctga 850  
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gacacagagc tgaaccgtcg ccgcccggcg ttctgcagca aagttgaggg 950  
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gcaggaacc gacccaatta cctgtacagg atgtgcgct ctctgctttc 1100  
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cagcctcact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300  
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 gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtgta 2150  
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 tccaagggga gggttcccc gtcaccaaac ccggttcctg agttaaaagt 2300  
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 cctgaggggtg gggctggctc ttactcagga aactgctgtg cccaacccat 2550  
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 cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650  
 caaagctgga taagttggtc attgattaaa aaaggagaag ccctctggga 2700  
 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
 Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala  
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 Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr  
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 Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu  
 35 40 45  
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
 50 55 60  
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
 65 70 75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
 80 85 90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
 95 100 105



Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu	110	115	120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val	125	130	135
Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe		395	400	405
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr		410	415	420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu		425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly		440	445	450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys		455	460	465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg		470	475	480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val		485	490	495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly		500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val		515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala		530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu		545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr		560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp		575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp		590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe		605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro		620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu		635	640	645
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr		650	655	660

<210> 89

<211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 89  
gatggcaaaa cgtgtgtttg acacg 25

<210> 90  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 90  
cctcaaccag gccacgggcc ac 22

<210> 91  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 91  
cccaggcaga gatgcagtac aggc 24

<210> 92  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
cctccagtag gtggatggat tggctc 26

<210> 93  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94  
<211> 3037  
<212> DNA  
<213> Homo sapiens

<400> 94

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actggaaatt tgttgtctag tggttgtggg tgaataaagg agggcagaat 150  
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200  
gttacgtggc cggaatcatt cccttggtg ttaatttctc agaggaacga 250  
ctgaagctgg tgactgtttt gggtgctggc cttctctgtg gaactgctct 300  
ggcagtcacg gtgcctgaag gagtacatgc ctttatgaa gatattcttg 350  
agggaaaaca ccaccaagca agtgaaacac ataatgtgat tgcacagac 400  
aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450  
cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500  
tcatgttgct ggtggaccag attggttaact cccatgtgca ttctactgac 550  
gatccagaag cagcaaggtc tagcaattcc aaaatcacca ccacgctggg 600  
tctggttgtc catgctgcag ctgatggtgt tgctttggga gcagcagcat 650  
ctacttcaca gaccagtgtc cagttaattg tgtttggtgc aatcatgcta 700  
cataaggcac cagctgcttt tggactgggt tccttcttga tgcagctgg 750  
cttagagcgg aatcgaatca gaaagcactt gctgggtcttt gcattggcag 800  
caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa 850  
gaagcccttt cagaggtgaa cgccacggga gtggccatgc ttttctctgc 900  
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 ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95  
 <211> 307  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
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 Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe  
                     20                    25                    30  
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
                     35                    40                    45  
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His  
                     50                    55                    60  
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
                     65                    70                    75  
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
                     80                    85                    90  
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His  
                     95                    100                    105  
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
                     110                    115                    120  
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp  
                     125                    130                    135  
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
                     140                    145                    150  
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
                     155                    160                    165  
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
                     170                    175                    180  
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
                     185                    190                    195  
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
                     200                    205                    210

Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	
				215					220					225	
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val	
				230					235					240	
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu	
				245					250					255	
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly	
				260					265					270	
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg	
				275					280					285	
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile	
				290					295					300	
Leu	Ser	Val	Gly	His	Gln	His									
				305											

<210> 96  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 96  
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<210> 97  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 97  
 ctgtgctcat gttcatggac aactg 25

<210> 98  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 98  
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<210> 99  
 <211> 1429

<212> DNA  
<213> Homo sapiens

<400> 99

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
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Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
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Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
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Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
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Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
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Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
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Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
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Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
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Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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Gly Gly Arg Gly Phe Gly Gly Ala Gly	Glu Leu Gly Gln Thr Pro	
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Gln Val Gln Ala Ala Leu Ser Val Ser	Gln Glu Asn Pro Glu Met	
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Glu Gly Pro Glu Arg Asp Gln Leu Val	Ile Pro Asp Gly Gln Glu	
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Glu Glu Gln Glu Ala Ala Gly Glu Gly	Arg Asn Gln Gln Lys Leu	
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Arg Gly Glu Asp Asp Tyr Asn Met Asp	Glu Asn Glu Ala Glu Ser	
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala	Gly Asn Asp Arg Asn Ile	
365	370	375
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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	

Gln Leu Thr Ser	Ala Gly Arg Arg Val	Val Phe Met Gly Asp Asp	170	175	180
Thr Trp Lys Asp	Leu Phe Pro Gly Ala	Phe Ser Lys Ala Phe Phe	185	190	195
Phe Pro Ser Phe	Asn Val Arg Asp Leu	Asp Thr Val Asp Asn Gly	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp Asp	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His Lys	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln Met	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp Thr	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly Asp	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe Leu	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu Pro	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu Leu	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met Ala	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser Ala	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val Ser	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln Ala	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser Ala	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala Thr	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly Ala	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val Arg	440	445	450

Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys	455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys	470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile	485	490	495
Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu	500	505	510
Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe	515	520	525
Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala	530	535	540
Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe	545	550	555
Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala	560	565	570
Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val	575	580	585
Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu	590	595	600
Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg	605	610	615
His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu	620	625	630
Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr	635	640	645
Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met	650	655	660
Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala	665	670	675
Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg	680	685	690
Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg	695	700	705
Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala	710	715	720
Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu	725	730	735

Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp Tyr	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met	Gln Glu Glu Phe Arg Gly	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	1010	1015	1020



Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
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Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
				1040					1045					1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
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Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
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Arg	Gln	Leu	Phe	Leu	Ala	Gln	Gln	Arg						
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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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<213> Homo sapiens

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				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
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Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
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Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser  
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Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly  
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro  
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly  
425 430 435

Leu Tyr Val Gln Met Glu Asn  
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<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

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<210> 107

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<212> DNA

<213> Artificial Sequence

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<400> 107

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                   20                  25                  30  
 Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
                   35                  40                  45  
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
                   50                  55                  60  
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
                   65                  70                  75  
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
                   80                  85                  90  
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
                   95                  100                 105  
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
                  110                 115                 120  
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
                  125                 130                 135  
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
                  140                 145                 150  
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
                  155                 160                 165  
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
                  170                 175                 180  
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
                  185                 190                 195  
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg

200	205	210
Arg Gly Phe Cys Ser Ala Asp Ser Gly	Gly Pro Leu Val Cys Arg	
215	220	225
Asn Arg Ala His Gly Leu Val Ser Phe	Ser Gly Leu Trp Cys Gly	
230	235	240
Asp Pro Lys Thr Pro Asp Val Tyr Thr	Gln Val Ser Ala Phe Val	
245	250	255
Ala Trp Ile Trp Asp Val Val Arg Arg	Ser Ser Pro Gln Pro Gly	
260	265	270
Pro Leu Pro Gly Thr Thr Arg Pro Pro	Gly Glu Ala Ala	
275	280	

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<211> 24

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<220>

<223> Synthetic oligonucleotide probe

<400> 112

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<220>

<223> Synthetic oligonucleotide probe

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cgagaaggaa acgaggccgt gag 23

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<212> DNA

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<211> 1808

<212> DNA

<213> Homo sapiens

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<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

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				20					25					30

Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly
				35					40					45

Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg
				50					55					60

Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys
				65					70					75

Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His
				80					85					90

Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg
				95					100					105

Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile
				110					115					120

Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr
				125					130					135

Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His
				140					145					150

Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala
				155					160					165

Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly
				170					175					180

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn
				185					190					195
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe
				200					205					210
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val
				215					220					225
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
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Arg

<210> 117

<211> 2249

<212> DNA

<213> Homo sapiens

<400> 117

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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

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				20					25					30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	
				35					40					45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	
				50					55					60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	
				65					70					75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	
				80					85					90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	
				95					100					105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	
				110					115					120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	
				125					130					135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	
				140					145					150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	
				155					160					165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	
				170					175					180	

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr  
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Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp  
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Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His  
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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<400> 121

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<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

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gaatcgggcc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
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cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
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aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400  
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<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

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				20					25					30
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly



170										175					180				
Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn					
				185					190					195					
Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val					
			200						205					210					
Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile					
			215						220					225					
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly					
			230						235					240					
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr					
			245						250					255					
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp					
			260						265					270					
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly					
			275						280					285					
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn											
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<210> 124

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 124

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<210> 125

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gacagagtgc tccatgatga tgtcc 25

<210> 126

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150  
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgtgctc 250  
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
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acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450  
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<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
			20						25					30

Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35						40					45

Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
			50						55					60

Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
			65						70					75

Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
			80						85					90

Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
			95						100					105

Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
			110						115					120

Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
			125						130					135

Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
			140						145					150

Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
			155						160					165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

170					175					180				
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185					190					195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200					205					210
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
				215					220					225
Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys
				230					235					240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser
				245					250					255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu
				260					265					270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser
				275					280					285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu
				290					295					300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His
				305					310					315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp
				320					325					330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr
				335					340					345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu
				350					355					360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu
				365					370					375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr
				380					385					390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp
				395					400					405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp
				410					415					420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu
				425					430					435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu
				440					445					450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys

455

460

465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
 470 475 480

Pro Val Ser Gln

<210> 129

<211> 2213

<212> DNA

<213> Homo sapiens

<400> 129

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 aaagaaggag atggtgttat ctgaaaagggt tagtcagctg atggaatgga 150  
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 gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgtct 250  
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
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<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

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Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln

20										25					30				
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met					
				35					40					45					
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys					
				50					55					60					
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile					
				65					70					75					
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys					
				80					85					90					
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg					
				95					100					105					
Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp					
				110					115					120					
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser					
				125					130					135					
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg					
				140					145					150					
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln					
				155					160					165					
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val					
				170					175					180					
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu					
				185					190					195					
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met					
				200					205					210					
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys					
				215					220					225					
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg					
				230					235					240					
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn					
				245					250					255					
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His					
				260					265					270					
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu					
				275					280					285					
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys					
				290					295					300					
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser					

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Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr					
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Ser Phe Leu Met Ser					
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<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
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 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250  
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 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550  
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600  
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 agaatacaga caaagcagta aactgggttaa gaaaggaagc aattaattac 700  
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 tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000  
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050  
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100



gcatgtacga ggctagtgc catgttccgc ttttgatgat gggaccagga 1150  
attaaagccg gcctacaagt atcaaagtgtg gtttctcttg tggatattta 1200  
ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250  
gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300  
gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350  
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cctattcgga tgggtgcatca atattgcctc aactctttga tctttcctcg 1450  
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aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132  
<211> 536  
<212> PRT  
<213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala	
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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	
				20					25					30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	
				35					40					45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	
				50					55					60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	
				65					70					75	
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	

Tyr Ser Ser Tyr	Thr Lys Asn Cys Thr	Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn	Ile Arg Ala Phe Tyr	Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met	Leu Gly Glu Ile Ile	Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln	Lys Thr Ile Val Ile	Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met	Glu His Arg Gln Phe	Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala	His Val Pro Leu Leu	Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu	Gln Val Ser Asn Val	Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met	Leu Asp Ile Ala Gly	Ile Pro Leu Pro Gln Asn	365	370	375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	380	385	390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	395	400	405
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	410	415	420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	425	430	435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	440	445	450
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	455	460	465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	470	475	480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	485	490	495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	500	505	510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	515	520	525
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val	530	535	

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133

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tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100  
gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
ctacatccta ggccttctgg ggcttttggg cacactggtt gccatgctgc 200  
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
gttggtcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
catcaccagc tgtgacatct atagcaccct tctgggcctg cccgctgaca 350  
tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctccctccctg 400  
gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450  
atcccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500  
ttggaggcct cctgggatcc attcctgttg cctggaatct tcatgggata 550  
ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600  
tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650  
ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700  
tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750  
gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
cagggatatgt gtgaagaacc aggggccaga gctggggggg ggctgggtct 850  
gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900  
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ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000  
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gctccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100  
agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150  
ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200  
ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250  
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300

cctccaaaga aactgattgg ccttgaacc tccatccac tcttggtatg 1350

actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400

tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450

gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
1				5					10					15

Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25					30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40					45

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
				50					55					60

Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala
				65					70					75

Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile
				80					85					90

Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr
				95					100					105

Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala
				110					115					120

Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro
				125					130					135

Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro
				140					145					150

Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr
				155					160					165

Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile
				170					175					180

Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr
				185					190					195

Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg
				200					205					210

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser  
 215 220 225

Leu Thr Gly Tyr Val  
 230

<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

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 aagtcacgcg tcccgctggc tcagaacctat ggctgtgcca gccggcaccc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgtt gttacaatga 200  
 cgccatcgtg tccctgagcg agaccgcga atgtgggtccc ccctgcacct 250  
 tctggccctg ctttgagctc tgctgtcttg attccttttg cctcaciaaac 300  
 gattttgttg tgaagctgaa gggtcagggt gtgaattccc agtgccactc 350  
 atctcccatc tccagtaaag gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaattttac aaaatgatgc 500  
 agtccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtggtttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136

<211> 119

<212> PRT

<213> Homo sapiens

<400> 136

Met	Val	Pro	Arg	Ile	Phe	Ala	Pro	Ala	Tyr	Val	Ser	Val	Cys	Leu
1				5					10					15
Leu	Leu	Leu	Cys	Pro	Arg	Glu	Val	Ile	Ala	Pro	Ala	Gly	Ser	Glu
				20					25					30
Pro	Trp	Leu	Cys	Gln	Pro	Ala	Pro	Arg	Cys	Gly	Asp	Lys	Ile	Tyr
				35					40					45
Asn	Pro	Leu	Glu	Gln	Cys	Cys	Tyr	Asn	Asp	Ala	Ile	Val	Ser	Leu
				50					55					60
Ser	Glu	Thr	Arg	Gln	Cys	Gly	Pro	Pro	Cys	Thr	Phe	Trp	Pro	Cys

	65		70		75
Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe					
	80		85		90
Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser					
	95		100		105
Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro					
	110		115		

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
 ctccactgca accaccaga gccatggctc cccgaggctg catcgtagct 50  
 gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100  
 agtggcccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250  
 ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgca ctcagcccg accctcgatg acaggctttg tcgcagtgtc 350  
 agctaattga acatcagggg aacgatgact cctggattct ccttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450  
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
 gacctgtctg agggccacc tgacgtgcc ctgaggaggc ccacaggtcc 550  
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600  
 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700  
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
 tatgtacttt ataaatgaaa a 771

<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys  
 1 5 10 15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	
				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
				35					40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
 gggggcgggg gcttgagca cggcgctggg gccgcccga gcgctcactc 50  
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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
 tctcttctg gctggtccc taggtccggt ggcagccttc aaggctgcca 250  
 cgccgtattc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300  
 tgcaggctct tgggcctgt ggacaaaggg cacgatgtga ccttctacaa 350  
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400  
 ggcccatccg caacctcacg ttccaggacc ttcacctgca ccatggaggc 450  
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500  
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
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 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650  
 aggcaaagat gcaccatcca actgtgtggt gtaccatcc tcctcccagg 700  
 atagtgaata catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750



ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800  
 ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850  
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900  
 ataccgagg ccaaagtcag gcacccccctg tcctatgtgg cccagcggca 950  
 gccttctgag tctggggcgc atctgctttc ggagcccagc accccccctgt 1000  
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050  
 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggtt ggctctgtga 1150  
 gtggcctcct tggcctcggc cctgggtccc tcctcctgc tctgggctca 1200  
 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
 atggggatgc tggacggctc agccccgtt ccaaggattt tggggtgctg 1300  
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450  
 tggggccacc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500  
 ccccgtaggc gccttggctc ccccgttttg cccgaggtg ctcttctgtc 1550  
 agacttctc tttgtaccac agtggctctg gggccaggcc tgccctgcca 1600  
 ctggccatcg ccacctccc cagctgcctc ctaccagcag tttctctgaa 1650  
 gatctgtcaa caggttaagt caatctgggg ctccactgc ctgcattcca 1700  
 gtcccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750  
 tggcctccgt gagcaaatgg tgtcttgggc aatctgaggc caggacagat 1800  
 gttgccccac ccaactggaga tggctgtgag ggaggtgggt ggggccttct 1850  
 gggaaggatga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900  
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140

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Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	
				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp					
	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile					
	305		310		

<210> 141

<211> 1732

<212> DNA

<213> Homo sapiens

<400> 141

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<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20					25					30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35					40					45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50					55					60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65					70					75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80					85					90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95					100					105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110					115					120

Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro	125	130	135
Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys	140	145	150
Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro	155	160	165
Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu	170	175	180
Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg	185	190	195
His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly	200	205	210
Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe	215	220	225
Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val	230	235	240
Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly	245	250	255
Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg	260	265	270
Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly	275	280	285
Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys	290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro	305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg	320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser	335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala	350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu	365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His	380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala	395	400	405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro  
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Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala  
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Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys  
 440 445 450

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
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 tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
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 1 5 10 15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30

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				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90

Arg Ser Pro

<210> 145

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 145

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atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
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<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20				25					30	

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35				40					45	

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



50										55					60				
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala					
				65					70					75					
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu					
				80					85					90					
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro					
				95					100					105					
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys					
				110					115					120					
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys					
				125					130					135					
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg					
				140					145					150					
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln					
				155					160					165					
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala					
				170					175					180					
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala					
				185					190					195					
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr					
				200					205					210					
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro					
				215					220					225					
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln					
				230					235					240					
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser					
				245					250					255					
Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala					
				260					265					270					
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala					
				275					280					285					
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys					
				290					295					300					
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro					
				305					310					315					
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr					
				320					325					330					
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile					

	335		340		345
Gln Cys Ser Phe Asp Ala Ser Gly Thr	Leu Thr Pro Glu Arg Ala				
350	355	360			
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr	Gly Ala His Ala Ser Leu				
365	370	375			
Arg Tyr Asn Pro Arg Glu Arg Gln Leu	Tyr Ala Trp Asp Asp Gly				
380	385	390			
Tyr Gln Ile Val Tyr Lys Leu Glu Met	Arg Lys Lys Glu Glu Glu				
395	400	405			

Val

<210> 147

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 147

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 aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

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Leu Val Gly Glu	Asp Ala Ala Phe	Ser Cys Phe Leu	Ser Pro Lys
	35	40	45
Thr Asn Ala Glu	Ala Met Glu Val	Arg Phe Phe Arg	Gly Gln Phe
	50	55	60
Ser Ser Val Val	His Leu Tyr Arg	Asp Gly Lys Asp	Gln Pro Phe
	65	70	75
Met Gln Met Pro	Gln Tyr Gln Gly	Arg Thr Lys Leu	Val Lys Asp
	80	85	90
Ser Ile Ala Glu	Gly Arg Ile Ser	Leu Arg Leu Glu	Asn Ile Thr
	95	100	105
Val Leu Asp Ala	Gly Leu Tyr Gly	Cys Arg Ile Ser	Ser Ser Gln Ser
	110	115	120
Tyr Tyr Gln Lys	Ala Ile Trp Glu	Leu Gln Val Ser	Ala Leu Gly
	125	130	135
Ser Val Pro Leu	Ile Ser Ile Thr	Gly Tyr Val Asp	Arg Asp Ile
	140	145	150
Gln Leu Leu Cys	Gln Ser Ser Gly	Trp Phe Pro Arg	Pro Thr Ala
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln	Asp Leu Ser Thr	Asp Ser Arg
	170	175	180
Thr Asn Arg Asp	Met His Gly Leu	Phe Asp Val Glu	Ile Ser Leu
	185	190	195
Thr Val Gln Glu	Asn Ala Gly Ser	Ile Ser Cys Ser	Met Arg His
	200	205	210
Ala His Leu Ser	Arg Glu Val Glu	Ser Arg Val Gln	Ile Gly Asp
	215	220	225
Thr Phe Phe Glu	Pro Ile Ser Trp	His Leu Ala Thr	Lys Val Leu
	230	235	240
Gly Ile Leu Cys	Cys Gly Leu Phe	Phe Gly Ile Val	Gly Leu Lys
	245	250	255
Ile Phe Phe Ser	Lys Phe Gln Trp	Lys Ile Gln Ala	Glu Leu Asp
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala	Glu Leu Arg Asp	Ala Arg Lys
	275	280	285
His Ala Val Glu	Val Thr Leu Asp	Pro Glu Thr Ala	His Pro Lys

290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val		
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val		
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp		
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His		
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr		
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr		
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe		
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg		
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn		
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu		
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu		
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu		
485	490	495
Pro Arg Gly Glu Met		
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<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

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<210> 150

<211> 23

<212> DNA  
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<220>  
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<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
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<220>  
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<400> 151  
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<210> 152  
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<212> DNA  
<213> Homo sapiens

<400> 152  
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accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400  
caccctctt tgggcgactg ctggaccctc ttccaccacc ttccaggcgc 450  
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acctctcagg cgcgcgaccg acccgcgcgc accacccttt cgacgaccac 550  
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agaccacagg gcagtgtgag tgtcggccag gttatcagg gttcactgt 800

gaaacctgca aagagggcctt ttacctaaat tacacttctg ggctctgtca 850  
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900  
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950  
aaaaggctgc tactctcaag gaccatactg gtttaaaca aggaggatga 1000  
gggtcataga ttacaaaaat attttatata cttttattct cttactttat 1050  
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atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300  
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tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200

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<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30

Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45

Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60

Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75

Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90

Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105

Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120

Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135

Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150

Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165

Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180

Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195

Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210

Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225

Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240



Cys	Gln	Pro	Cys	Asp	Cys	Ser	Pro	His	Gly	Ala	Leu	Ser	Ile	Pro
				245					250					255

Cys Asn Arg

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 154  
 aactgctctg tggttggaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 156  
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgcggcgag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50  
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 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150  
 ccgggaaaag ggctttgcc tggagaagga catgaagaac gtcgtggggg 200  
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgcca tcattctcac tcagctggag 400  
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600  
 gggctcctgtg acctcggccca gtgtccaccc acctcgctca gcggctcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158

<211> 163

<212> PRT

<213> Homo sapiens

<400> 158

Met	Gly	Gly	Leu	Leu	Leu	Ala	Ala	Phe	Leu	Ala	Leu	Val	Ser	Val
1				5					10					15

Pro	Arg	Ala	Gln	Ala	Val	Trp	Leu	Gly	Arg	Leu	Asp	Pro	Glu	Gln
			20						25					30

Leu	Leu	Gly	Pro	Trp	Tyr	Val	Leu	Ala	Val	Ala	Ser	Arg	Glu	Lys
			35						40					45

Gly	Phe	Ala	Met	Glu	Lys	Asp	Met	Lys	Asn	Val	Val	Gly	Val	Val
			50						55					60

Val	Thr	Leu	Thr	Pro	Glu	Asn	Asn	Leu	Arg	Thr	Leu	Ser	Ser	Gln
			65						70					75

His	Gly	Leu	Gly	Gly	Cys	Asp	Gln	Ser	Val	Met	Asp	Leu	Ile	Lys
			80						85					90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105

Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120

Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135

Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150

Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln
			155						160			

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150  
gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttacc 200  
tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250  
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300  
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggtctct 450  
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
gtgagcaggg gacacccct atgatctct ggataggac ctccgtgtcc 600  
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gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctggg 700  
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgc 850  
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ctgcagagca aagccacatc aggagtgact cagggggtgg tcgggggagc 1100  
tggagccaca gccctggtct tctgtcctt ctgcgtcatc ttcgtttag 1150  
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250  
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

cttctgccccg ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350  
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 caccgagtagc tcggagatca agatccacag atgagaaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaacact 1550  
 atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600  
 tcaaacctga atccacactg tgcctccct tttatttttt taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	1	5	10	15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	20	25	30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	50	55	60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	65	70	75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	80	85	90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	95	100	105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	110	115	120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	125	130	135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	140	145	150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	155	160	165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	170	175	180	

Ile Gly Thr Ser Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg Ser
185	190 195
Ser Val Leu Thr Leu Ile Pro Gln Pro	Gln Asp His Gly Thr Ser
200	205 210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala	Ser Val Thr Thr Asn
215	220 225
Lys Thr Val His Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu Thr
230	235 240
Met Thr Val Phe Gln Gly Asp Gly Thr	Val Ser Thr Val Leu Gly
245	250 255
Asn Gly Ser Ser Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg Leu
260	265 270
Val Cys Ala Val Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg Leu
275	280 285
Ser Leu Ser Trp Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro Ser
290	295 300
Asn Pro Gly Val Leu Glu Leu Pro Trp	Val His Leu Arg Asp Ala
305	310 315
Ala Glu Phe Thr Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln Gln
320	325 330
Val Tyr Leu Asn Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly Val
335	340 345
Thr Gln Gly Val Val Gly Gly Ala Gly	Ala Thr Ala Leu Val Phe
350	355 360
Leu Ser Phe Cys Val Ile Phe Val Val	Val Arg Ser Cys Arg Lys
365	370 375
Lys Ser Ala Arg Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile Glu
380	385 390
Asp Ala Asn Ala Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu Thr
395	400 405
Glu Pro Trp Ala Glu Asp Ser Pro Pro	Asp Gln Pro Pro Pro Ala
410	415 420
Ser Ala Arg Ser Ser Val Gly Glu Gly	Glu Leu Gln Tyr Ala Ser
425	430 435
Leu Ser Phe Gln Met Val Lys Pro Trp	Asp Ser Arg Gly Gln Glu
440	445 450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile	Lys Ile His Arg
455	460

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgccttcac 100  
 cctggaggag gaggatatca cagggaacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttcggag gacaggaggc ccaggaaggt gtccccagtg 200  
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250  
 gagggaggat cgggtgatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagcacca 400  
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500  
 tcggaggagg acattttcac gcccctgcag acgggaagct gcgttcccg 550  
 acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcct 650  
 gctccacccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
   1                  5                  10                  15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr  
                   20                  25                  30  
 Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg  
                   35                  40                  45  
 Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly  
                   50                  55                  60  
 Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile  
                   65                  70                  75

Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr  
80 85 90

Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro  
95 100 105

Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly  
110 115 120

Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr  
125 130 135

Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys  
140 145 150

Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser  
155 160 165

Cys Val Pro Glu His  
170

<210> 163

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

gtcctccgga aagtccttat c 21

<210> 166

<211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
gcctagtgtt cggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
caggacctg gtacgtgaag gccatgggtg tcgataagga cttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 168  
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169  
gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50  
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150  
gtagggggag agaccaggat catcaagggg ttcgagtga agcctcactc 200  
ccagccctgg caggcagccc tgctcgagaa gacgcggcta ctctgtggg 250  
cgacgtcat cgtcccccaga tggctcctga cagcagcca ctgcctcaag 300  
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggagg 350  
ctgtgagcag acccgacag cactgagtc cttccccac ccgggttca 400  
acaacagcct cccaacaaa gaccaccga atgacatcat gctggtgaag 450  
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cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggtga ctccgggggc cctctggtct gtaaccagtc ttttcaaggc 750
attatctcct ggggccagga tccgtgtgcy atcacccgaa agcctggtgt 800
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acaattagac tggacccacc caccacagcc catcacctc catttccact 900
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cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
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tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
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aaaa 1204

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<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

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<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
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Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
             20             25             30
His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
             35             40             45
Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
             50             55             60
Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
             65             70             75
Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
             80             85             90
Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
             95             100            105

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Asp His Arg Asn Asp Ile Met Leu Val	Lys Met Ala Ser Pro Val	
110	115	120
Ser Ile Thr Trp Ala Val Arg Pro Leu	Thr Leu Ser Ser Arg Cys	
125	130	135
Val Thr Ala Gly Thr Ser Cys Leu Ile	Ser Gly Trp Gly Ser Thr	
140	145	150
Ser Ser Pro Gln Leu Arg Leu Pro His	Thr Leu Arg Cys Ala Asn	
155	160	165
Ile Thr Ile Ile Glu His Gln Lys Cys	Glu Asn Ala Tyr Pro Gly	
170	175	180
Asn Ile Thr Asp Thr Met Val Cys Ala	Ser Val Gln Glu Gly Gly	
185	190	195
Lys Asp Ser Cys Gln Gly Asp Ser Gly	Gly Pro Leu Val Cys Asn	
200	205	210
Gln Ser Leu Gln Gly Ile Ile Ser Trp	Gly Gln Asp Pro Cys Ala	
215	220	225
Ile Thr Arg Lys Pro Gly Val Tyr Thr	Lys Val Cys Lys Tyr Val	
230	235	240
Asp Trp Ile Gln Glu Thr Met Lys Asn	Asn	
245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

ggctgcggga ctggaagtca tcggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

cctctgggtct gtaaccag 18

<210> 174

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 174

tctgtgatgt tgccggggta ggcg 24

<210> 175

<211> 25

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<213> Artificial Sequence

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<400> 175

cgtgtagaca ccaggctttc gggcg 25

<210> 176

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca etc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

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aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150  
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aaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

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Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	155	160	165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	170	175	180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	200	205	210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				215	220	

<210> 181

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

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<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 183

cctttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 184

gatgtctgcc accccaag 18

<210> 185

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 185

gcatacctgat atgacttgtc acgtggc 27

<210> 186

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 186

tacaagaggg aagaggagtt gcac 24

<210> 187

<211> 52

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 187

gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

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ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

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20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
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<210> 190  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 191  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
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<210> 193  
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<212> DNA  
<213> Homo sapiens

<400> 193  
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gactttggaa gtgaccacc atgggggtca gcatcttttt gctcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
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<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

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Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	200	205	210
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	215	220	225
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	230	235	240
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<211> 1485

<212> DNA

<213> Homo sapiens

<400> 195

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<210> 196  
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 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu  
 35 40 45  
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp  
 50 55 60  
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met  
 65 70 75

Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys  
80 85 90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr  
95 100 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu  
110 115 120

Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro  
125 130 135

Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro  
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<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

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 acagtccctg ggggtgtcac caggctgcaa gtctgcacc gtgtgcaagc 4100  
 acggcctgtg ccgctccgtg gagaaggaca gcgtggtgtg cgagtgcgc 4150  
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 cggccacaga tgccaccatg gaaaatgtgt ggcaactggg acctcataca 4250  
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 gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcc 4350  
 catctcagac caaggggagc cctactgcct gtgccagccc ggcttttagcg 4400  
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 gcccatcatg gaatgtcgtg ggggctgtgg gcccagtgcc tgccagccca 4550  
 cccgcagcaa gcggcggaac tacgtcttcc agtgcacgga cggctcctcg 4600  
 tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgttcc 4650  
 ctaagcccct gcccgcctgc ctgccacctc tcggactcca gcttgatgga 4700  
 gttgggacag ccatgtggga cccctggtg attcagcatg aaggaaatga 4750  
 agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800  
 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198  
 <211> 1523  
 <212> PRT  
 <213> Homo sapiens

<400> 198  
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 1 5 10 15  
 Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro  
 20 25 30  
 Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

35	40	45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro		
50	55	60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg		
65	70	75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu		
80	85	90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe		
95	100	105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys		
110	115	120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu		
125	130	135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg		
140	145	150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp		
155	160	165
Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu		
170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg		
185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu		
200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp		
215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr		
230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp		
245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro		
260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr		
275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu		
290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu		
305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr		



320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser	Lys Asn Gln Ile Ser Asp	
335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu	Lys Ser Leu Thr Ser Leu	
350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu	Ile Ala Lys Gly Leu Phe	
365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu	Leu Leu Asn Ala Asn Lys	
380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe	Gln Asp Leu Gln Asn Leu	
395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys	Leu Gln Thr Ile Ser Lys	
410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile	Gln Thr Leu His Leu Ala	
425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His	Leu Lys Trp Leu Ala Asp	
440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr	Ser Gly Ala Arg Cys Ser	
455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser	
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu	Asp Tyr Arg Ser Arg Phe	
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg	
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg	
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn	
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys	
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys	
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu	
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val	
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn	

605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser		
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr		
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu		
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly		
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys		
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala		
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln		
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val		
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met		
740	745	750
Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr		
755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile		
770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe		
785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg		
800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu		
815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu		
830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly		
845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu		
860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser		
875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr		

890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly	Thr
920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro	Tyr
935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys	Ile
950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr	Cys His Leu Ser Asp	Ser
965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu	Gly
980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp	Cys
995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val	Cys
1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val	Ile
1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu	Cys Gln His Glu Ala	Lys
1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser	Cys Glu Cys Val Pro	Gly
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp	Asn Asp Asp Cys Val	Ala
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys	Val Asp Thr Ile Asn	Gly
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe	Ser Gly Pro Phe Cys	Glu
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln	Thr Ser Pro Cys Asp	Gln
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys	Ile Val Val Gln Gln	Glu
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe	Ala Gly Pro Arg Cys	Glu
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly	Lys Asp Ser Tyr Val	Glu
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln	Ala Asn Ile Ser Leu	Gln

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
1520		

<210> 199  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 199  
 atggagattc ctgccaactt gccg 24

<210> 200  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 200  
 ttgttgcat tgaggaggag cagc 24

<210> 201  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 201  
 gagggcatcg tcgaaatag cctagaacag aactccatca aagccatccc 50

<210> 202  
 <211> 753  
 <212> DNA  
 <213> Homo sapiens

<400> 202  
 ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
 gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150  
 cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
 atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
 caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
 agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
 gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400  
 gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
 atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
 caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
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 ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
 cctgtgtcat cttgtccgt ttcctcccaa tattccttct caaacttga 700  
 gagggaaaat taagctatac ttttaagaaa ataaatattt ccattttaa 750  
 gtc 753

<210> 203

<211> 148

<212> PRT

<213> Homo sapiens

<400> 203

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1				5					10					15
Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
				110					115					120

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
140 145

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

gcaggctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

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<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

ctacactcgt tgcaaaactgg caaaaatatt ctcgagggtt ggcctgg 47

<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

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tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatctt actgtcactt cccagatctg cttctcacca 250  
agagagattc ttttcttaaa cgactatata gggccccaat tgactggata 300  
gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350  
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
ctgatgtcct ctatccatct ctaaatgtca ccagctttga ctgagttgtt 450  
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgtctgt 500  
ctccatcaac agatacgaaa ggaagaaaaa totgactttg gactggaag 550  
ccctagtaca gctgcgtgga agattgacat cccaagattg ggagagggtt 600  
catctgatcg tggcagggtg ttatgacgag agagtcctgg agaattgtga 650  
acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
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ttatggattg tagaccagtt tttgaaacca aaaaagaaac ctagaatcta 1150



atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200  
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
 tttatgctat aatcattcca aattttgccca gtgttaagtt acaaagtgg 1300  
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 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
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 tcactgtcat ctgttaggga atttttgttt gtctgtctt tgctgggac 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp				

155	160	165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg		
170	175	180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val		
185	190	195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe		
200	205	210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val		
215	220	225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu		
230	235	240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly		
245	250	255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu		
260	265	270
Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg		
275	280	285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg		
290	295	300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr		
305	310	315
Arg Tyr Val Thr Lys Leu Leu Val		
320		

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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tctacctota tccggcttcc agacaagctg caggaattcc agggattact 150

ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200

tttgcgatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250

ccttctggtt tggcaggcgc ctcttggtta gtttgggcac tgttgatgta 300

ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350

gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
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 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaagga accttaatga ccaacagatc ctagaagaca 850  
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
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 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250  
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 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
 ttaa 1554

<210> 212  
 <211> 462  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu  
 1 5 10 15

Val Gly Ala Val	Leu Tyr Leu Tyr	Pro Ala Ser Arg	Gln Ala Ala	
	20	25	30	
Gly Ile Pro Gly	Ile Thr Pro Thr	Glu Glu Lys Asp	Gly Asn Leu	
	35	40	45	
Pro Asp Ile Val	Asn Ser Gly Ser	Leu His Glu Phe	Leu Val Asn	
	50	55	60	
Leu His Glu Arg	Tyr Gly Pro Val	Val Ser Phe Trp	Phe Gly Arg	
	65	70	75	
Arg Leu Val Val	Ser Leu Gly Thr	Val Asp Val Leu	Lys Gln His	
	80	85	90	
Ile Asn Pro Asn	Lys Thr Ser Asp	Pro Phe Glu Thr	Met Leu Lys	
	95	100	105	
Ser Leu Leu Arg	Tyr Gln Ser Gly	Gly Gly Ser Val	Ser Glu Asn	
	110	115	120	
His Met Arg Lys	Lys Leu Tyr Glu	Asn Gly Val Thr	Asp Ser Leu	
	125	130	135	
Lys Ser Asn Phe	Ala Leu Leu Leu	Lys Leu Ser Glu	Glu Leu Leu	
	140	145	150	
Asp Lys Trp Leu	Ser Tyr Pro Glu	Thr Gln His Val	Pro Leu Ser	
	155	160	165	
Gln His Met Leu	Gly Phe Ala Met	Lys Ser Val Thr	Gln Met Val	
	170	175	180	
Met Gly Ser Thr	Phe Glu Asp Asp	Gln Glu Val Ile	Arg Phe Gln	
	185	190	195	
Lys Asn His Gly	Thr Val Trp Ser	Glu Ile Gly Lys	Gly Phe Leu	
	200	205	210	
Asp Gly Ser Leu	Asp Lys Asn Met	Thr Arg Lys Lys	Gln Tyr Glu	
	215	220	225	
Asp Ala Leu Met	Gln Leu Glu Ser	Val Leu Arg Asn	Ile Ile Lys	
	230	235	240	
Glu Arg Lys Gly	Arg Asn Phe Ser	Gln His Ile Phe	Ile Asp Ser	
	245	250	255	
Leu Val Gln Gly	Asn Leu Asn Asp	Gln Gln Ile Leu	Glu Asp Ser	
	260	265	270	
Met Ile Phe Ser	Leu Ala Ser Cys	Ile Ile Thr Ala	Lys Leu Cys	
	275	280	285	
Thr Trp Ala Ile	Cys Phe Leu Thr	Thr Ser Glu Glu	Val Gln Lys	
	290	295	300	

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
				305					310					315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320					325					330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335					340					345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350					355					360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365					370					375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380					385					390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395					400					405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410					415					420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425					430					435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440					445					450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455					460						

<210> 213  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50  
 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100  
 tcagggttg tgccctctcg cttctgacg ctctggcgc atctggtggt 150  
 cgtcacacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
 gccgcgtct ctgtaccct gggcctcttt gcagtggagc tggccggttt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400  
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450

agctgtcaact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600  
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
tgttttgtag taacattaag acttatatac agtttttaggg gacaattaa 750  
aaaaaaaa 759

<210> 214  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 214  
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
1 5 10 15  
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
20 25 30  
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
35 40 45  
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
50 55 60  
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
65 70 75  
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
80 85 90  
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
95 100 105  
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
110 115 120  
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
125 130 135  
Lys Lys Lys Pro Phe  
140

<210> 215  
<211> 697  
<212> DNA  
<213> Homo sapiens

<400> 215  
tcccggaacc tgccgcctg ccactatgtc ccgcgcctct atgctgcttg 50

cctgggctct cccagcctc ctgcgactcg gagcggctca ggagacagaa 100  
 gacccggcct gctgcagccc catagtgcc cggaacgagt ggaagggcct 150  
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450  
 ccaggccatc cgggcagccc agggctctact ggctgcgggt gtggctcagg 500  
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
 ctaccgctcc cctgagggcc ctgctgatcc gcacccatt cctccctcc 650  
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1				5					10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
			20						25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
			35						40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
			50						55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
			65						70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
			80						85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
			95						100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
			110						115					120

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217  
 <211> 1871  
 <212> DNA  
 <213> Homo sapiens

<400> 217  
 ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50  
 gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100  
 tctatctggt catctgtggc caggatgatg gtccctcccg ctcagaggac 150  
 cctgagcgtg atgaccacga gggccagccc cgccccggg tgccctcgaa 200  
 gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250  
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300  
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaat 350  
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400  
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450  
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500  
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550  
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600  
 gaacggggcc gccggacctc gctttgcacc cacgaccag ccaagatctg 650  
 ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700  
 tcaaagtcgt ctgtgtctac atgccttct acagcacgga ctatcggctg 750  
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800  
 cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850



ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900  
 gttgggcctc aggcagggag gggggtggag acgaggagat gccaagtggg 950  
 gccagggcca agtctcaagt ggcagagaaa ggggcccaag tgctgggtccc 1000  
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050  
 ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100  
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150  
 gtcattgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200  
 gcaacagggg gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250  
 atggatggct gagagggctt cctaggagcc agtcagcagg gtgggggtggg 1300  
 gccagaggag ctctccagcc ctgcctagtg ggcgcctga gcccttgtc 1350  
 gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400  
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450  
 ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500  
 cccatcctta agctaagaca ggacgattgt ggtcctccca cactaaggcc 1550  
 acagcccatc cgcgtgctgt gtgtccctct tccaccccaa cccctgctgg 1600  
 ctccctctggg agcatccatg tcccgagag gggccctca acagtcagcc 1650  
 tcacctgtca gaccgggggt ctcccggatc tggatggcgc cgcctctca 1700  
 gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc 1750  
 tgttctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800  
 aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850  
 aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
1					5				10					15

Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20					25					30

Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	215	220	225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	230	235	240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				245	250	

<210> 219  
 <211> 2065  
 <212> DNA  
 <213> Homo sapiens

<400> 219  
 gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50  
 gcaggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100  
 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150  
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200

gcgccgcgcgc cgccgtcgtc cctgcagcgc tgtcgacctc gccgctagca 250  
tcttcccagag caccggggtc ccggggtagg aggcgacgcg ggcgagcacc 300  
agcgccagcc ggctgcggct gccacacgg ctcaccatgg gctccgggcg 350  
ccgggcgctg tccgcgggtg cggccgtgct gctggtcctc acgctgccgg 400  
ggctgcccgct ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
aagtgtctgg tgggtgtgca ctggaacccg gccacggact ccaagggtc 500  
ctcttctctc ccgctgggga tatcggtccg ggccggccaac tccaaggctc 550  
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600  
aagacgcgca tcatttactt cgatcagatc ctggatgaatg tgggtaattt 650  
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700  
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccagggttaac 750  
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800  
tggtactcgt gaagctgcc cgaatggtgt cctgctctac ctagataaag 850  
aggataaggt ttacctaaaa ctggagaaaag gtaatttggt tggaggctgg 900  
cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950  
ttctccatga tgttcatcca ggtgagggat gacccactcc tgagttattg 1000  
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
gggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100  
tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150  
aagcagataa tacctatgct taaatgtaac agtcaaaaagc tgtctgcaag 1200  
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250  
gaattttatt tgtttagttt taaaagactg gcaaccaggt ctaaggatta 1300  
gaaaactcta aagtctgac ttcaatcaac ggtagtgtg atactgcca 1350  
agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400  
ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450  
aactggatt atgttttctc ttaaaataag gtaatgaatg gcttgccac 1500  
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550  
gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600  
ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

aaagttgctt acccaaaatc taagtgtc atccctgagc ctcagcaaaa 1700  
 cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750  
 aatgattgat aataaccact ttattaaaaa cctaagggtt tttttttttc 1800  
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850  
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900  
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaaa 1950  
 ttcaaataat ccatatctaa atttagtgca atatcttgtc ttttgtatag 2000  
 gtcatatgaa ttcataaaat tatttatgct tgttatagaa taaagattaa 2050  
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
1				5				10						15
Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
			20					25						30
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
			35					40						45
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
			50					55						60
Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala
			65					70						75
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr
			80					85						90
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe
			95					100						105
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr
			110					115						120
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile
			125					130						135
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe
			140					145						150
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val
			155					160						165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
185 190 195

Phe Leu Val Phe Pro Leu  
200

<210> 221  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 221  
acggctcacc atgggctccg 20

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 222  
aggaagagga gcccttggag tccg 24

<210> 223  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 223  
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224  
<211> 902  
<212> DNA  
<213> Homo sapiens

<400> 224  
cgggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50  
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100  
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150  
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200

ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
 tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300  
 gtgaagggtt gaagagtata aaccaggtg agacagcacc ctctatgcga 350  
 ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400  
 ttcttttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450  
 ttcatggaga ttctctcaa ttcttcttt attcagcttt catgacgctg 500  
 gtcattatct tgctgcatgt attctggggc attgtatatt ttgatggctg 550  
 tgagaagaaa aagtggggca tcttcttat cgttctctg acccacctgc 600  
 tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650  
 tcagcattta taatcctggg gctcatgggc acctgggcat tcttagctgc 700  
 gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750  
 actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800  
 tcccaaaccg cagactacat ctttagagga agcacaactg tgcttttttc 850  
 tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900  
 ta 902

<210> 225  
 <211> 257  
 <212> PRT  
 <213> Homo sapiens

<400> 225  
 Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly  
 1 5 10 15  
 Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu  
 20 25 30  
 Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser  
 35 40 45  
 Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile  
 50 55 60  
 Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly  
 65 70 75  
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 Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn  
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Pro Gly Glu Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser
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Asp Ser Pro Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val
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Cys Glu Lys Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
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Trp Ala Phe Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
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<211> 3939

<212> DNA

<213> Homo sapiens

<400> 226

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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser
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Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln
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Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val
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Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg
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Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro
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Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser

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Asp Leu Asp Asn	Asn Val Ala Phe Ile	Gly Met Tyr Gln Thr Met	
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Asn Ser Phe Tyr	Val Val Val Val Val	Lys Thr Glu Asp Gln Ala	
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Ile Asp Arg Ala	Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala	
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Ala Gly Thr Gly	Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe	
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Glu Pro Val Gly	Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val	
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Pro Asn Tyr Thr	Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr	Met
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Cys Ile Arg Gln	Cys Ser Gly Pro Leu	Tyr Val Asp Arg Met	Val
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Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe					
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<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
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Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
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Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
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Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
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His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
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Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
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				305					310					315					
Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn					
				320					325					330					
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile					
				335					340					345					
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala					
				350					355					360					
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr					



365										370					375				
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala					
				380					385					390					
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu					
				395					400					405					
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met					
				410					415					420					
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val					
				425					430					435					
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile					
				440					445					450					
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro					
				455					460					465					
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu					
				470					475					480					
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr					
				485					490					495					
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val					
				500					505					510					
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser					
				515					520					525					
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly					
				530					535					540					
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val					
				545					550					555					
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu					
				560					565					570					
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr					
				575					580					585					
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu					
				590					595					600					
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly					
				605					610					615					
Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp					
				620					625					630					
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu					
				635					640					645					
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His					

	650		655		660
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser			
	665		670		675
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val			
	680		685		690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr			
	695		700		705
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile Ile			
	710		715		720
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val			
	725		730		735
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg			
	740		745		750
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val			
	755		760		765
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile			
	770		775		780
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp			
	785		790		795
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val			
	800		805		

<210> 230

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

cgccttaccg cgcagcccga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

cctgagctgt aaccccactc cagg 24

<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttcctgag 250  
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agattggaca ttogtttgaa aaccggccga tgtatgtact gaagttcagc 500  
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile	1	5	10	15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn	20	25	30	
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn	35	40	45	
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala	65	70	75	
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr	80	85	90	
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met	95	100	105	
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr	110	115	120	
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn	125	130	135	
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly	140	145	150	
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr	155	160	165	
Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195	

Arg Lys Ile Val	Ser Asp Tyr Gln Arg	Asp Pro Ala Ile Thr Ser
200	205	210
Ile Leu Glu Lys	Met Asp Ile Phe Leu	Leu Pro Val Ala Asn Pro
215	220	225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln	Asn Arg Leu Trp Arg Lys
230	235	240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser	Cys Ile Gly Ala Asp Pro
245	250	255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala	Gly Lys Gly Ala Ser Asp
260	265	270
Asn Pro Cys Ser	Glu Val Tyr His Gly	Pro His Ala Asn Ser Glu
275	280	285
Val Glu Val Lys	Ser Val Val Asp Phe	Ile Gln Lys His Gly Asn
290	295	300
Phe Lys Gly Phe	Ile Asp Leu His Ser	Tyr Ser Gln Leu Leu Met
305	310	315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys	Ala Pro Asp Ala Glu Glu
320	325	330
Leu Asp Lys Val	Ala Arg Leu Ala Ala	Lys Ala Leu Ala Ser Val
335	340	345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro	Thr Cys Thr Thr Val Tyr
350	355	360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp	Ala Tyr Asp Asn Gly Ile
365	370	375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg	Asp Thr Gly Thr Tyr Gly
380	385	390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile	Pro Thr Ala Glu Glu Thr
395	400	405
Trp Leu Gly Leu	Lys Thr Ile Met Glu	His Val Arg Asp Asn Leu
410	415	420

Tyr

<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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cccgcccttc ctccacaaag agcacccttg cctcacaggt gtattccctc 200  
aacaccgact ttgccttccg cctataccgc aggctgggtt tggagacccc 250  
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agaagacca agggaagggt gtagacataa tccaaggcct tgaccttctg 650  
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gccctttcac cttgaatata caagaaagaa cttcccatte ctggtgggcg 750  
agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800  
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<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
1				5					10					15

Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
				20					25					30

Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
				35					40					45

Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
				50					55					60

Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
				65					70					75

Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
				80					85					90

Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
				95					100					105

Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
				110					115					120

Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
				125					130					135

Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
				140					145					150

Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
				155					160					165

Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
				170					175					180

Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
				185					190					195

Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala
				200					205					210



Lys Trp Glu Lys	Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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 cgtggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850  
 tgagaaacac ctttaacaca gctgtctacc accctcatgg cctcaaccat 1900  
 ggccttggtc caggccctgg agggaaatcat ggagcccccc acaggcccag 1950  
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 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25					30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40					45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55					60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70					75	
Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80				85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95				100					105	

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	110	115	120
Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val	125	130	135
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala	140	145	150
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala	155	160	165
Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala	170	175	180
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	185	190	195
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	200	205	210
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala	215	220	225
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	230	235	240
Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala	245	250	255
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	260	265	270
Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	275	280	285
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	290	295	300
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	305	310	315
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala	320	325	330
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	335	340	345
Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala	350	355	360
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380	385	390

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150  
ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200  
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300  
ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350  
tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400  
gaagcagaga agcttggcca tggggtaaac aacgctgctg gacaggccgg 450  
gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500  
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caggctggaa aggaagtgga gaagcttggc caaggtgcc accatgctgc 600  
tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800

acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
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 tacacca 957

<210> 248  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 248  
 Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu  
 1 5 10 15  
 Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu  
 20 25 30  
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg  
 35 40 45  
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His  
 50 55 60  
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met  
 65 70 75  
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu  
 80 85 90  
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile  
 95 100 105  
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn  
 110 115 120  
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln  
 125 130 135  
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys  
 140 145 150  
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu  
 155 160 165  
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala  
 170 175 180  
 Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
 185 190 195  
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
 200 205 210  
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly



	215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg			
	230	235	240

Ser Val Ala Asn Ile Met Pro  
245

<210> 249  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 249  
caatatgcat cttgcacgtc tgg 23

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
aagcttctct gcttcctttc ctgc 24

<210> 251  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
tgacccatt gagaaggat ttgaaggat caaccgaggg ctg 43

<210> 252  
<211> 3781  
<212> DNA  
<213> Homo sapiens

<400> 252  
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tgaccctgac tcaactccagg tccggaggcg ggggccccgc gggcgactcg 150  
  
ggggcgacc gcggggcgga gctgccgcc gtgagtccgg ccgagccacc 200  
  
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250

ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300  
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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile	
				125					130					135	
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly	
				140					145					150	
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn	
				155					160					165	
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp	
				170					175					180	
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala	
				185					190					195	
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe	
				200					205					210	
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro	
				215					220					225	
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe	
				230					235					240	
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly	
				245					250					255	
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	
				260					265					270	
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	
				275					280					285	
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	
				290					295					300	
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	
				305					310					315	
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	
				320					325					330	
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	
				335					340					345	
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	
				350					355					360	
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys	
				365					370					375	
Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Pro	
				380					385					390	
Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg	
				395					400					405	

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val	665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro	680	685	690

Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
				695					700					705	
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
				710					715					720	
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
				725					730					735	
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
				740					745					750	
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
				755					760					765	
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
				770					775					780	
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
				785					790					795	
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
				800					805					810	
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
				815					820					825	
Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val				
				830					835						

<210> 254

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 254

agcccgtagca gaatctgctc ctgg 24

<210> 255

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

tgaagccagg gcagcgtcct ctgg 24

<210> 256

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<213> Artificial Sequence

<220>  
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<400> 256  
gtacaggctg cagttggc 18

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<400> 258  
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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				35					40					45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
				50					55					60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
				80					85					90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
				140					145					150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
				155					160					165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
				170					175					180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
				185					190					195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
				215					220					225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	
				245					250					255	
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	
				260					265					270	
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	

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Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala					
				290					295					300					
Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu					
				305					310					315					
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg					
				320					325					330					
Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser					
				335					340					345					
Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro					
				350					355					360					
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu					
				365					370					375					
Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly					
				380					385					390					
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu					
				395					400					405					
Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala					
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Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly					
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Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp					
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Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val					
				455					460					465					
Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile					
				470					475					480					
Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys					
				485					490					495					
Arg	Ile	Asn	Gln	Glu	Ser	Gly	Ser	Leu	Ser	Phe	Leu	Ser	Asn	Ser					
				500					505					510					
Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu					
				515					520					525					
His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu					
				530					535					540					
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu					
				545					550					555					
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu					

560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val Glu	
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met Gln	
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu Glu	
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe Cys	
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys Arg	
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile Phe	
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro Ser	
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg Asn	
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val Arg	
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu Asp	
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr Phe	
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val Phe	
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu Gly	
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu Met	
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<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261  
gtgccactac ggggtgtgga cgac 24

<210> 262  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 262  
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<210> 263  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60

Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75

Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90



Thr Asn Pro Ile	Ser Glu Glu Thr Thr	Thr Phe Pro Thr Gly Gly
95		100 105
Phe Thr Pro Glu	Ile Gly Lys Lys Lys	His Thr Glu Ser Thr Pro
110		115 120
Phe Trp Ser Ile	Lys Pro Asn Asn Val	Ser Ile Val Leu His Ala
125		130 135
Glu Glu Pro Tyr	Ile Glu Asn Glu Glu	Pro Glu Pro Glu Pro Glu
140		145 150
Pro Ala Ala Lys	Gln Thr Glu Ala Pro	Arg Met Leu Pro Val Val
155		160 165
Thr Glu Ser Ser	Thr Ser Pro Tyr Val	Thr Ser Tyr Lys Ser Pro
170		175 180
Val Thr Thr Leu	Asp Lys Ser Thr Gly	Ile Glu Ile Ser Thr Glu
185		190 195
Ser Glu Asp Val	Pro Gln Leu Ser Gly	Glu Thr Ala Ile Glu Lys
200		205 210
Pro Glu Glu Phe	Gly Lys His Pro Glu	Ser Trp Asn Asn Asp Asp
215		220 225
Ile Leu Lys Lys	Ile Leu Asp Ile Asn	Ser Gln Val Gln Gln Ala
230		235 240
Leu Leu Ser Asp	Thr Ser Asn Pro Ala	Tyr Arg Glu Asp Ile Glu
245		250 255
Ala Ser Lys Asp	His Leu Lys Arg Ser	Leu Ala Leu Ala Ala Ala
260		265 270
Ala Glu His Lys	Leu Lys Thr Met Tyr	Lys Ser Gln Leu Leu Pro
275		280 285
Val Gly Arg Thr	Ser Asn Lys Ile Asp	Asp Ile Glu Thr Val Ile
290		295 300
Asn Met Leu Cys	Asn Ser Arg Ser Lys	Leu Tyr Glu Tyr Leu Asp
305		310 315
Ile Lys Cys Val	Pro Pro Glu Met Arg	Glu Lys Ala Ala Thr Val
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Phe Asn Thr Leu	Lys Asn Met Cys Arg	Ser Arg Arg Val Thr Ala
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Leu Leu Lys Val	Tyr	
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<210> 266  
 <211> 2403  
 <212> DNA

<213> Homo sapiens

<400> 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
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Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20				25					30	

Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu

	35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe	50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser	65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp	80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr	95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile	110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly	125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile	140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg	170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile	185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu	200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu	215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu	230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile	245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys	290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro	305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val			

320	325	330
Val Ala Ser Gln Gly Phe Gln Ala Gly	Arg His Tyr Trp Glu Val	
335	340	345
Asp Val Gly Gln Asn Val Gly Trp Tyr	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Gly Lys Asn Asn Val	Thr Leu Ser Pro Asn Asn	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Thr Thr	Glu His Leu Tyr Phe Thr	
380	385	390
Phe Asn Pro His Phe Ile Ser Leu Pro	Pro Ser Thr Pro Pro Thr	
395	400	405
Arg Val Gly Val Phe Leu Asp Tyr Glu	Gly Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Thr Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Leu Thr Cys	
425	430	435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr	Ile Gln His Ala Met Tyr	
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Asp Glu Glu Lys Gly Thr Pro Ile Phe	Ile Cys Pro Val Ser Trp	
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<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
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 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
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gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaacct 750  
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catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900  
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aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900

tccagaaaga agccaagata tatkcttatt ttcatttcca aacaactact 1950  
 atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000  
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050  
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 cca 2103

<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 269

Met	Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys	1	5	10	15
Trp	Glu	Pro	Trp	Val	Ile	Gly	Leu	Val	Ile	Phe	Ile	Ser	Leu	Ile	20	25	30	
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	

Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
 215 220 225  
 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro  
 230 235 240  
 Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys  
 245 250 255  
 Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys  
 260 265 270  
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser  
 275 280 285  
 Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp  
 290 295 300  
 Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly  
 305 310 315  
 Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg  
 320 325 330  
 Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro  
 335 340 345  
 Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly  
 350 355 360  
 Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly  
 365 370 375  
 Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly  
 380 385 390  
 Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly  
 395 400 405  
 Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys  
 410 415 420

Thr Gly Ile

<210> 270  
 <211> 1170  
 <212> DNA  
 <213> Homo sapiens

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 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150



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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

Met	Leu	Gly	Ser	Pro	Cys	Leu	Leu	Trp	Leu	Leu	Ala	Val	Thr	Phe
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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
				20				25					30	

Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35				40						45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	50	55	60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	65	70	75
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			230	235	

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200

gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgctgtctct 250

acgccctcaa tctgtctttt tggttaatgt ccatcagtgt gttggcagtt 300

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<210> 273  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<400> 273  
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                     20                    25                    30  
 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu  
                     35                    40                    45  
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe  
                     50                    55                    60  
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile  
                     65                    70                    75  
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu  
                     80                    85                    90  
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys  
                     95                    100                    105  
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met  
                     110                    115                    120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	
				125					130					135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	
				140					145					150	
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	
				155					160					165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	
				170					175					180	
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	
				185					190					195	
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	
				200					205					210	
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	
				215					220					225	
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	
				230					235					240	
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	
				245					250					255	
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	
				260					265					270	
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	
				275					280					285	
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	
				290					295					300	
Glu	Met	Glu	Glu	Leu											
				305											

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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cgggcagcct ctccacttca tcccgaggaa gcagctgtgt gacggagagc 450  
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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	110	115	120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	125	130	135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	170	175	180	

Gly Ser Leu Val	Ser Leu His Cys Leu	Ala Cys Gly Lys Ser	Leu
	185	190	195
Lys Thr Pro Arg	Val Val Gly Gly Glu	Glu Ala Ser Val Asp	Ser
	200	205	210
Trp Pro Trp Gln	Val Ser Ile Gln Tyr	Asp Lys Gln His Val	Cys
	215	220	225
Gly Gly Ser Ile	Leu Asp Pro His Trp	Val Leu Thr Ala Ala	His
	230	235	240
Cys Phe Arg Lys	His Thr Asp Val Phe	Asn Trp Lys Val Arg	Ala
	245	250	255
Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala	Lys
	260	265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn	Asp
	275	280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly	Thr
	290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr	Pro
	305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln	Asn
	320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln	Val
	335	340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly	Glu
	350	355	360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly	Val
	365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln	Ser
	380	385	390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly	Cys
	395	400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala	Tyr
	410	415	420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys	Ala Glu Leu	
	425	430	

<210> 276  
 <211> 3143  
 <212> DNA  
 <213> Homo sapiens



<400> 276

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<210> 277  
 <211> 761  
 <212> PRT  
 <213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	

Gly Thr Met Asn	Asn Phe Leu Gly Ser	Glu Pro Ile Leu Met Arg
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Thr Leu Gly Ser	Gln Pro Val Leu Lys	Thr Asp Asn Phe Leu Arg
215		220 225
Trp Leu His His	Asp Ala Ser Phe Val	Ala Ala Ile Pro Ser Thr
230		235 240
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe Asp
245		250 255
Phe Phe Glu Arg	Leu His Thr Ser Arg	Val Ala Arg Val Cys Lys
260		265 270
Asn Asp Val Gly	Gly Glu Lys Leu Leu	Gln Lys Lys Trp Thr Thr
275		280 285
Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu Pro
290		295 300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro
305		310 315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val
320		325 330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp
335		340 345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu
350		355 360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg
365		370 375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr
380		385 390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly Thr
395		400 405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val
410		415 420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr
425		430 435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly
440		445 450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp
455		460 465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala
470		475 480

Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg	Ala
485		490	495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg
500		505	510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu
515		520	525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg
530		535	540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser
545		550	555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala
560		565	570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala
575		580	585
Leu Ala Ser Tyr	Tyr Trp Ser His Gly	Pro Ala Ala Val Pro	Glu
590		595	600
Ala Ser Ser Thr	Val Tyr Asn Gly Ser	Leu Leu Leu Ile Val	Gln
605		610	615
Asp Gly Val Gly	Gly Leu Tyr Gln Cys	Trp Ala Thr Glu Asn	Gly
620		625	630
Phe Ser Tyr Pro	Val Ile Ser Tyr Trp	Val Asp Ser Gln Asp	Gln
635		640	645
Thr Leu Ala Leu	Asp Pro Glu Leu Ala	Gly Ile Pro Arg Glu	His
650		655	660
Val Lys Val Pro	Leu Thr Arg Val Ser	Gly Gly Ala Ala Leu	Ala
665		670	675
Ala Gln Gln Ser	Tyr Trp Pro His Phe	Val Thr Val Thr Val	Leu
680		685	690
Phe Ala Leu Val	Leu Ser Gly Ala Leu	Ile Ile Leu Val Ala	Ser
695		700	705
Pro Leu Arg Ala	Leu Arg Ala Arg Gly	Lys Val Gln Gly Cys	Glu
710		715	720
Thr Leu Arg Pro	Gly Glu Lys Ala Pro	Leu Ser Arg Glu Gln	His
725		730	735
Leu Gln Ser Pro	Lys Glu Cys Arg Thr	Ser Ala Ser Asp Val	Asp
740		745	750
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<210> 278  
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 281  
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<212> DNA  
<213> Homo sapiens

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<210> 282

<211> 523

<212> PRT

<213> Homo sapiens

<400> 282

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30

Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45

Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60

Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75

Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90

Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105

Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120

Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135

Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150

Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile



155	160	165
Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro 170	175	180
Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met 185	190	195
Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe 200	205	210
Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile 215	220	225
Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu 230	235	240
Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe 245	250	255
Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly 260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn 275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu 290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu 305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys 320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn 335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His 350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile 365	370	375
Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu 380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys 395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu 410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser 425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser		

440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr		
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp		
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu		
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala		
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr		
515	520	

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 283  
 tgcctttgct cacctacccc aagg 24

<210> 284  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 284  
 tcaggctggt ctccaaagag aggg 24

<210> 285  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 285  
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286  
 <211> 2340  
 <212> DNA  
 <213> Homo sapiens

<400> 286  
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ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100  
cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150  
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
tgctgtcact gcatgctctg ccaaggagga gggaaactgca gtgacagcag 300  
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400  
ccaggagagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450  
gggttgcaga gcccctcagc catgttggga gccaaagccac actggctacc 500  
aggtccccta cacagtcccg ggctgccctt gggtctgggtg cttctggccc 550  
tgggggccgg gtggggccag gaggggtcag agcccgtcct gctggagggg 600  
gagtgcctgg tggctctgtga gcctggccga gctgctgcag gggggcccg 650  
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tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750  
ggggccatct acttcgacca ggtcctgggtg aacgagggcg gtggctttga 800  
ccgggcctct ggctccttcg tagccctgt ccgggggtgtc tacagcttcc 850  
ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900  
atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950  
gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000  
accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050  
tactcaagtt tctctggctt cctcatcttc cctctctgag gaccaagtc 1100  
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cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250  
gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300  
ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350  
ggcaaggttt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400  
ctccggttcc cccaccccag ctctctgctc aatgctgatc agggacaggt 1450

ggcgaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500  
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550  
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctaggggtggg 1600  
 aggctcagcc acaggcagaa ggggtgggaag ggccctggagt ctgtggctgg 1650  
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 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750  
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800  
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850  
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900  
 ccacctctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
 cactctgact gctgcctcct tctcccagc tctctcactg agttatcttc 2000  
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 cattccttca gacctctcc tgccagtatg ctaaaccctc cctctctctt 2150  
 tcttatcccg ctgtccatt ggcccagcct ggatgaatct atcaataaaa 2200  
 caactagaga atgggtgtca gtgagacact atagaattac taaggagaag 2250  
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300  
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
				200					205						

<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290

ctgtgtctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50

tagccgcccc gcctcgacgc cgtcccgga cccctgtgct ctgcgcgaag 100

ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200

ccgcctactc cggggctctg cgcggcgagc gtcaggccga ggctgaccgg 250

agccagcgct ctacaggagg acctgcgctg tcgcgcgagg ggtctgggag 300

atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350

tcacctggct caataggtcc aaggtggaaa agcagctaca ggtcatctca 400

gtgctccagt gggctctgtc ctctcttgta ctgggagtggt cctgcagtgc 450

catcctcatg tacatattct gcactgattg ctggctcatc gctgtgctct 500

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ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact 650

atatcttttg ataccacccc catggtatca tgggcctggg tgccttctgc 700

aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750

gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800

agtacctgat gtctggaggt atctgccctg tcagccggga caccatagac 850

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gggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950

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 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350  
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 tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttatttaaaa 1450  
 gaaattataa caattttgct aaacaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550  
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292

<211> 388

<212> PRT

<213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	

Val Ser Lys Lys Phe Pro Gly Ile Arg	Pro Tyr Leu Ala Thr Leu
185	190 195
Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser	
200	205 210
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu	
215	220 225
Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly	
230	235 240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr	
245	250 255
Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly	
260	265 270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	
275	280 285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	
290	295 300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	
305	310 315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	
320	325 330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	
335	340 345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	
350	355 360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	
365	370 375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn	
380	385

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

gggcggcgagg atggggggccg ggggcggcg ggcgcgcact cgctgaggcc 50  
ccgacgcagg gccggggccg gccagggcc gaggagcgcg gcggccagag 100  
cggggcccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150  
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccaact 200  
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caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300  
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cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
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cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550  
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aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750  
gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800  
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 ttgttctgtt gccagggctg gactacagtg gcacagtctt ggctcactgc 2650  
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 agctgtatct ttttgtatct tgtattttgt agctgtagt tttgtatttt 2750  
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 agctcaagt atctgcctgc ttcagcctcc caaagtgtg ggattacaga 2850  
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 aaaaccacct gattcaaaat gggcagagg gccgggtgtg gccccaacta 2950  
 ccaggagagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000  
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050  
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
1				5					10					15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
			20						25					30
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
			35						40					45
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
			50						55					60
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
			65						70					75
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala

80	85	90
Val Ile Ile Leu Asn His Asn Phe Glu 95	Ile Asp Phe Leu Cys Gly 100	
Trp Thr Met Cys Glu Arg Phe Gly Val 110	Leu Gly Ser Ser Lys Val 115	
Leu Ala Lys Lys Glu Leu Leu Tyr Val 125	Pro Leu Ile Gly Trp Thr 130	
Trp Tyr Phe Leu Glu Ile Val Phe Cys 140	Lys Arg Lys Trp Glu Glu 145	
Asp Arg Asp Thr Val Val Glu Gly Leu 155	Arg Arg Leu Ser Asp Tyr 160	
Pro Glu Tyr Met Trp Phe Leu Leu Tyr 170	Cys Glu Gly Thr Arg Phe 175	
Thr Glu Thr Lys His Arg Val Ser Met 185	Glu Val Ala Ala Ala Lys 190	
Gly Leu Pro Val Leu Lys Tyr His Leu 200	Leu Pro Arg Thr Lys Gly 205	
Phe Thr Thr Ala Val Lys Cys Leu Arg 215	Gly Thr Val Ala Ala Val 220	
Tyr Asp Val Thr Leu Asn Phe Arg Gly 230	Asn Lys Asn Pro Ser Leu 235	
Leu Gly Ile Leu Tyr Gly Lys Lys Tyr 245	Glu Ala Asp Met Cys Val 250	
Arg Arg Phe Pro Leu Glu Asp Ile Pro 260	Leu Asp Glu Lys Glu Ala 265	
Ala Gln Trp Leu His Lys Leu Tyr Gln 275	Glu Lys Asp Ala Leu Gln 280	
Glu Ile Tyr Asn Gln Lys Gly Met Phe 290	Pro Gly Glu Gln Phe Lys 295	
Pro Ala Arg Arg Pro Trp Thr Leu Leu 305	Asn Phe Leu Ser Trp Ala 310	
Thr Ile Leu Leu Ser Pro Leu Phe Ser 320	Phe Val Leu Gly Val Phe 325	
Ala Ser Gly Ser Pro Leu Leu Ile Leu 335	Thr Phe Leu Gly Phe Val 340	
Gly Ala Ala Ser Phe Gly Val Arg Arg 350	Leu Ile Gly Glu Ser Leu 355	
Glu Pro Gly Arg Trp Arg Leu Gln		

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 298  
cttcctctgt gggaggacca tgtg 24

<210> 299  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gccacctcca tgctaacgcg g 21

<210> 300  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 300  
ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301  
<211> 1334  
<212> DNA  
<213> Homo sapiens

<400> 301  
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tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150  
tcagtttggtc ttgtgggggt ggtggcaggc aggcgggctt acgcctgata 200  
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250  
tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300  
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350  
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450  
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 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600  
 ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650  
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 gttgtatggg ttgtgtctgt tccccagaat gccagctct gagctgctg 750  
 agggtaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800  
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850  
 aaatctctca gttcaccaga tgggtgtaggg ccagcattg taaattcaca 900  
 cgttgactgt gcttgtgaat tatctgggga tgcaggctct gattcagtag 950  
 gccaggttg ggcattctta aaaaactccc acgtgatgct gatgctggtc 1000  
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgac 1100  
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150  
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200  
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250  
 gcggagggtg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300  
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5					10					15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20					25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp

65

70

75

Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr  
80 85 90

Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln  
95 100 105

Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu  
110 115 120

Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr  
125 130 135

Cys Gly Val Leu Leu Ser Phe Leu  
140

<210> 303

<211> 1768

<212> DNA

<213> Homo sapiens

<400> 303

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tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200  
tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300  
ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350  
ctctcgctgg agcagtggcc tcaccaactg tctcacgtct ggaggcactg 400  
actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450  
tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500  
ggcgatggct cccactgccc aggcacacgc cttgctgtag tcaatcactg 550  
ccctggggcc aggacgggccc gtggacacct gctcagaagc agtgggtgag 600  
acatcacgct gcccgcceat ctaacctttt catgtcctgc acatcacctg 650  
atccatgggc taatctgaac tctgtcccga ggaaccaga gcttgagtga 700  
gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750  
acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800  
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gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900  
 ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950  
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000  
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050  
 ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100  
 ctcccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150  
 agcaagacat agctgacagg ggctaattggc tcagtgttgg cccaggaggt 1200  
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250  
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 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350  
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 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550  
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600  
 aggcattggt gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650  
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
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 aattatggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
1				5					10					15

Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20					25					30

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60

Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



65

70

75

Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala  
 80 85 90

Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly  
 95 100 105

Arg Arg Arg Asp

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

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 tgtcactgcc tcccgcgcgc tccgtcccgc gccatgaccc agccggtgcc 100  
 ccggctctcc gtgcccgcgc cgctggccct gggctcagcc gcaactgggcg 150  
 ccgccttcgc cactggcctc ttcctgggga ggcggtgccc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
 gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300  
 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350  
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 cgctgcccgc ggacgggcgc gtggtgacct gcgaggtgga cgcgcagccc 500  
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 cgaaagggga cgtggcgcc gagtgtgtgc gaaacctaaa cgaacgcata 800  
 cggcgggacg tcagggtcta catcagcctc ctgccoctgg gcgatggact 850  
 caccttgccc ttcaagatct agggctggcc cctagttagt gggctcgagg 900  
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306  
<211> 262  
<212> PRT  
<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala	
1				5					10					15	
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe	
			20						25					30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys	
				35					40					45	
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser	
				50					55					60	
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				65					70					75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
				80					85					90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
				95					100					105	
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	
				110					115					120	
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
				125					130					135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
				140					145					150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
				155					160					165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
				185					190					195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
				230					235					240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
				245					250					255	

Leu Thr Leu Ala Phe Lys Ile  
260

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcgc 150  
ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200  
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250  
aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300  
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cgccagtgag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400  
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 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcgccgtta 1650  
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 tcaagtcgcg ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750  
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 ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900  
 agcgcagagg acaaggagca cgaggagggt cgggactcgg aggaggggcc 1950  
 aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000  
 acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050  
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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

	35	40	45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro	50	55	60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys	65	70	75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala	80	85	90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala	95	100	105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp	110	115	120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala	125	130	135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser	140	145	150
Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser	155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala	170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu	185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala	200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys	215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser	230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser	245	250	255
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val	260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro	275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser	290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu	305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg			

320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu Gln	
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg Gly	
350	355	360
Glu Ala Glu Arg Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu Arg	
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser	
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg	
425	430	435
Pro Glu Glu Lys Gln Gln Ala Lys Pro	Val Lys Val Glu Arg Thr	
440	445	450
Arg Lys Arg Ser Glu Gly Phe Ser Met	Asp Arg Lys Val Glu Lys	
455	460	465
Lys Lys Glu Pro Ser Val Glu Glu Lys	Leu Gln Lys Leu His Ser	
470	475	480
Glu Ile Lys Phe Ala Leu Lys Val Asp	Ser Pro Asp Val Lys Arg	
485	490	495
Cys Leu Asn Ala Leu Glu Glu Leu Gly	Thr Leu Gln Val Thr Ser	
500	505	510
Gln Ile Leu Gln Lys Asn Thr Asp Val	Val Ala Thr Leu Lys Lys	
515	520	525
Ile Arg Arg Tyr Lys Ala Asn Lys Asp	Val Met Glu Lys Ala Ala	
530	535	540
Glu Val Tyr Thr Arg Leu Lys Ser Arg	Val Leu Gly Pro Lys Ile	
545	550	555
Glu Ala Val Gln Lys Val Asn Lys Ala	Gly Met Glu Lys Glu Lys	
560	565	570
Ala Glu Glu Lys Leu Ala Gly Glu Glu	Leu Ala Gly Glu Glu Ala	
575	580	585
Pro Gln Glu Lys Ala Glu Asp Lys Pro	Ser Thr Asp Leu Ser Ala	
590	595	600
Pro Val Asn Gly Glu Ala Thr Ser Gln	Lys Gly Glu Ser Ala Glu	

	605		610		615
Asp Lys Glu His	Glu Glu Gly Arg Asp	Ser Glu Glu Gly Pro Arg			
	620	625		630	
Cys Gly Ser Ser	Glu Asp Leu His Asp	Ser Val Arg Glu Gly Pro			
	635	640		645	
Asp Leu Asp Arg	Pro Gly Ser Asp Arg	Gln Glu Arg Glu Arg Ala			
	650	655		660	
Arg Gly Asp Ser	Glu Ala Leu Asp Glu Glu Ser				
	665	670			

<210> 309  
 <211> 3871  
 <212> DNA  
 <213> Homo sapiens

<400> 309  
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 ttcacatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150  
 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttggttc 200  
 ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250  
 taaaaagact tgctgctttc aaatagctgt attccctttt tgggttcac 300  
 agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350  
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 attatgtaaa ttagctggga aagatgcca tacagaatgt gcaaatttca 500  
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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu	
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Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro	
				50					55					60	
Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu	
				65					70					75	
Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile	
				80					85					90	
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile	
				95					100					105	
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala	
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Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu	
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala	
				140					145					150	
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu	
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Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg	
				170					175					180	
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met	
				185					190					195	
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly	
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Gly Ser Thr Ser Asp Lys Thr Ile Leu	Ser Arg Val Gly Arg Val	
275	280	285
Cys Lys Asn Asp Val Gly Gly Gln Arg	Ser Leu Ile Asn Lys Trp	
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Thr Thr Phe Leu Lys Ala Arg Leu Ile	Cys Ser Ile Pro Gly Ser	
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Asp Gly Ala Asp Thr Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr Leu	
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Leu Pro Thr Arg Asp Glu Arg Asn Pro	Val Val Tyr Gly Val Phe	
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Thr Thr Thr Ser Ser Ile Phe Lys Gly	Ser Ala Val Cys Val Tyr	
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Ser Met Ala Asp Ile Arg Ala Val Phe	Asn Gly Pro Tyr Ala His	
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Lys Glu Ser Ala Asp His Arg Trp Val	Gln Tyr Asp Gly Arg Ile	
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Pro Tyr Pro Arg Pro Gly Thr Cys Pro	Ser Lys Thr Tyr Asp Pro	
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Leu Ile Lys Ser Thr Arg Asp Phe Pro	Asp Asp Val Ile Ser Phe	
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Ile Lys Arg His Ser Val Met Tyr Lys	Ser Val Tyr Pro Val Ala	
425	430	435
Gly Gly Pro Thr Phe Lys Arg Ile Asn	Val Asp Tyr Arg Leu Thr	
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Gln Ile Val Val Asp His Val Ile Ala	Glu Asp Gly Gln Tyr Asp	
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Val Met Phe Leu Gly Thr Asp Ile Gly	Thr Val Leu Lys Val Val	
470	475	480
Ser Ile Ser Lys Glu Lys Trp Asn Met	Glu Glu Val Val Leu Glu	
485	490	495
Glu Leu Gln Ile Phe Lys His Ser Ser	Ile Ile Leu Asn Met Glu	
500	505	510
Leu Ser Leu Lys Gln Gln Gln Leu Tyr	Ile Gly Ser Arg Asp Gly	

515	520	525
Leu Val Gln Leu Ser 530	Leu His Arg Cys Asp Thr Tyr Gly Lys 535	Ala 540
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Gly Asn Ala Cys Ser 560	Arg Tyr Ala Pro Thr Ser Lys Arg Arg 565	Ala 570
Arg Arg Gln Asp Val 575	Lys Tyr Gly Asp Pro Ile Thr Gln Cys 580	Trp 585
Asp Ile Glu Asp Ser 590	Ile Ser His Glu Thr Ala Asp Glu Lys 595	Val 600
Ile Phe Gly Ile Glu 605	Phe Asn Ser Thr Phe Leu Glu Cys Ile 610	Pro 615
Lys Ser Gln Gln Ala 620	Thr Ile Lys Trp Tyr Ile Gln Arg Ser 625	Gly 630
Asp Glu His Arg Glu 635	Glu Leu Lys Pro Asp Glu Arg Ile Ile 640	Lys 645
Thr Glu Tyr Gly Leu 650	Leu Ile Arg Ser Leu Gln Lys Lys Asp 655	Ser 660
Gly Met Tyr Tyr Cys 665	Lys Ala Gln Glu His Thr Phe Ile His 670	Thr 675
Ile Val Lys Leu Thr 680	Leu Asn Val Ile Glu Asn Glu Gln Met 685	Glu 690
Asn Thr Gln Arg Ala 695	Glu His Glu Glu Gly Gln Val Lys Asp 700	Leu 705
Leu Ala Glu Ser Arg 710	Leu Arg Tyr Lys Asp Tyr Ile Gln Ile 715	Leu 720
Ser Ser Pro Asn Phe 725	Ser Leu Asp Gln Tyr Cys Glu Gln Met 730	Trp 735
His Arg Glu Lys Arg 740	Arg Gln Arg Asn Lys Gly Gly Pro Lys 745	Trp 750
Lys His Met Gln Glu 755	Met Lys Lys Lys Arg Asn Arg Arg His 760	His 765
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<220>

<223> Synthetic oligonucleotide probe

<400> 311

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<211> 24

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<223> Synthetic oligonucleotide probe

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<400> 313

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<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

<400> 314

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	35	40	45	
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	50	55	60	
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Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	110	115	120	
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	125	130	135	
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	140	145	150	



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 Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu  
 185 190 195  
 Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser  
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 Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln  
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<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg	
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Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro	
				20					25					30	
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu		
				35					40					45	
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	
				50					55					60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	
				65					70					75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	
				80					85					90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	
				95					100					105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	
				110					115					120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	
				125					130					135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu	
				140					145					150	
Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu	
				155					160					165	
Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile	
				170					175					180	
Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn	
				185					190					195	
Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala	
				200					205					210	
Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val	
				215					220					225	
Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg	
				230					235					240	
Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His	

245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val		
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala		
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn		
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu		
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu		
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys		
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala		
350	355	360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys		
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val		
380	385	390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser		
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr		
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro		
425	430	435
Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln		
440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro		
455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala		
470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys		
485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp		
500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro		
515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val		

530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg	Pro Val Pro Arg Asn Gly	
545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr	Arg Phe Arg Ser Cys Asn	
560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala	Leu Thr Phe Arg Glu Glu	
575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr	Asp Leu Phe Lys Ser Phe	
590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg	Tyr Thr Gly Val Ala Pro	
605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln	Ala Arg Ala Leu Gly Tyr	
620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val	Asp Gly Thr Pro Cys Ser	
635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln	Gly Arg Cys Ile His Ala	
650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys	Lys Lys Phe Asp Lys Cys	
665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly	Cys Ser Lys Gln Ser Gly	
680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr	Asn Asn Val Val Thr Ile	
695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val	Arg Gln Gln Gly Asn Pro	
710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu	Lys Leu Pro Asp Gly Ser	
725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu	Met Pro Ser Pro Thr Asp	
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu	Arg Tyr Ser Gly Ala Thr	
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His	Gly Pro Leu Ala Gln Pro	
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly	Asn Pro Gln Asp Thr Arg	
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg	Pro Thr Pro Ser Thr Pro	
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His	Arg Arg Ala Gln Ile Leu	

815

820

825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys  
 830 835

&lt;210&gt; 318

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 318

ccctgaagct gccagatggc tcc 23

&lt;210&gt; 319

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 319

ctgtgctctt cggcgcagcc agtc 24

&lt;210&gt; 320

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 320

ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

&lt;210&gt; 321

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 321

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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100

ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150

ttgtggactg gtgtttggta tcctggccct aactctaatt gtctgtttt 200

gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250

gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgatg 350



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 gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
 attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
 ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
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 atactgaaaa tggaatagaa tttgatcca tgctggatga gagaggttat 850  
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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu
1				5					10					15

Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30

Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
			35						40					45

Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60

Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75

Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe

80	85	90
Arg Ser Gly Asn Gly Thr Asp Glu Thr	Leu Glu Val His Asp Phe	
95	100	105
Lys Asn Gly Tyr Thr Gly Ile Tyr Phe	Val Gly Leu Gln Lys Cys	
110	115	120
Phe Ile Lys Thr Gln Ile Lys Val Ile	Pro Glu Phe Ser Glu Pro	
125	130	135
Glu Glu Glu Ile Asp Glu Asn Glu Glu	Ile Thr Thr Thr Phe Phe	
140	145	150
Glu Gln Ser Val Ile Trp Val Pro Ala	Glu Lys Pro Ile Glu Asn	
155	160	165
Arg Asp Phe Leu Lys Asn Ser Lys Ile	Leu Glu Ile Cys Asp Asn	
170	175	180
Val Thr Met Tyr Trp Ile Asn Pro Thr	Leu Ile Ser Val Ser Glu	
185	190	195
Leu Gln Asp Phe Glu Glu Glu Gly Glu	Asp Leu His Phe Pro Ala	
200	205	210
Asn Glu Lys Lys Gly Ile Glu Gln Asn	Glu Gln Trp Val Val Pro	
215	220	225
Gln Val Lys Val Glu Lys Thr Arg His	Ala Arg Gln Ala Ser Glu	
230	235	240
Glu Glu Leu Pro Ile Asn Asp Tyr Thr	Glu Asn Gly Ile Glu Phe	
245	250	255
Asp Pro Met Leu Asp Glu Arg Gly Tyr	Cys Cys Ile Tyr Cys Arg	
260	265	270
Arg Gly Asn Arg Tyr Cys Arg Arg Val	Cys Glu Pro Leu Leu Gly	
275	280	285
Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln	Gly Gly Arg Val Ile Cys	
290	295	300
Arg Val Ile Met Pro Cys Asn Trp Trp	Val Ala Arg Met Leu Gly	
305	310	315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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 cgttgatcac caccatcctg ccgcaactggc ggaggacagc gcacgtgggc 200  
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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
1					5				10				15	

Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

20	25	30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser		
35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly		
50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln		
65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu		
80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr		
95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu		
110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala		
125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro		
140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr		
155	160	165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu		
170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln		
185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala		
200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val		
215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val		
230	235	

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150

gcacgcgggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200

aaccccgctca cctccgtggt ccagtagcaa gggctctgga ggagctgcgt 250  
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gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350  
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gtacaccggc atgggtggga tggcgagac tgttcagacc aggtacacat 600  
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caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
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aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta 850  
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atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000  
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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30

Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45

Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60

Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75

Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90

Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105

Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120

Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135

Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150

Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val	
				155					160					165	
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val	
				170					175					180	
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala	
				185					190					195	
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser	
				200					205					210	
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe	
				215					220					225	
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile	
				230					235					240	
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro	
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<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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<211> 225  
<212> PRT  
<213> Homo sapiens

<400> 328

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Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	
				20					25					30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	
				35					40					45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	
				50					55					60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	
				65					70					75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	
				80					85					90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	
				95					100					105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	
				110					115					120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	
				125					130					135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	
				140					145					150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	
				155					160					165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	
				170					175					180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	
				185					190					195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	
				200					205					210	
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val	
				215					220					225	

<210> 329  
<211> 1315  
<212> DNA  
<213> Homo sapiens

<400> 329

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<210> 330  
 <211> 220  
 <212> PRT  
 <213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

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Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu

	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
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 agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200  
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<210> 334  
<211> 85  
<212> PRT  
<213> Homo sapiens

<400> 334  
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35 40 45  
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
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Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
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Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335  
<211> 742  
<212> DNA  
<213> Homo sapiens

<400> 335  
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<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

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Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser
				20					25					30

Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val
				35					40					45

Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu
				50					55					60

Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg
				65					70					75

Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met
				80					85					90

Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu
				95					100					105

Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln
				110					115					120

Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr
				125					130					135

Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr
				140					145			

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

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ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgaggggcggg 200

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 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500  
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 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600  
 tgtccacgag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650  
 cccggccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700  
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750  
 ttccccctgac cgccactctg ggccctggccg gcttcaccct gctcctcagt 800  
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 gccagccct gcgcgcgaga ggactcccgg gactggcgga gggcccgccc 1000  
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050  
 cgcactggga gtgggtcct ccgggctcggg catctgctgt cgctgcctcg 1100  
 gcccggggca gagccggggc gcccggggg cccgtcttag tgttctgccg 1150  
 gaggaccag ccgcctccaa tccctgacag ctcttgggc tgagttggg 1200  
 acgccaggtc ggtgggaggc tggatgaagg gagcggggag gggcagagga 1250  
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 aaaaaaaaa 1310

<210> 338  
 <211> 246  
 <212> PRT  
 <213> Homo sapiens

<400> 338  
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 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser  
 20 25 30  
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
 35 40 45



Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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caagacccta agaaccatca gccctcagct gcacctcctc ccctccaagg 150

atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag gggttactccc tgagtgactg gctgtgcctg 300  
 gctttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
 tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400  
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
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 agggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

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Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25				30	
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40				45	
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55				60	
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70				75	
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85				90	
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100				105	
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115				120	
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130				135	

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg  
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtccct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln	
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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
				110					115					120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe	545	550	555

Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val  
560 565 570

Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln  
575 580 585

His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser  
590 595 600

Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu  
605 610 615

Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe  
620 625 630

Asp Gln Ile Asn Ala Val Asp Glu Arg  
635

<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

ggagagggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

tatgtcgctg cgagggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2524

<212> DNA

<213> Homo sapiens



<400> 351

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tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcatact cccctcgaac cccaccagcc ccagcccgcc ccccggtgctc 200  
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

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						20			25					30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135  
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
 140 145 150  
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
 155 160 165  
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
 170 175 180  
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
 185 190 195  
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
 200 205 210  
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
 215 220 225  
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
 230 235 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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cggccaggat ggcatacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggggttc tggccccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcggtcgc tggggcccgg cgctatcgcg gccatcgtga 350  
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser  
 1 5 10 15  
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu  
 20 25 30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
 35 40 45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
 50 55 60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
 65 70 75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
 80 85 90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
 95 100 105  
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
 110 115 120  
 Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
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gtgcctgacg gcggcgctgg cccacggctg tctgcaactgc cacagcaact 150  
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtccctgg 200  
tggttggtggc acatccccgt gtcagggggc ctgctcaccg actggagcga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300  
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggtat ttcccaacg agctgcgaaa 400  
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acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500  
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550  
agtagcccc agaggcgctg ggagtgttg caccgccctc cctgaagtt 600  
tgctccatct cacgtgggg gtcaacctgg ggacccttc cctccgggc 650  
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tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactgc 750  
acgtgcctg ctttggctat aactgcgagt agggctcagg catcacacc 800  
acctgtcca gggccctact gtccctgggg tcccaggctc tccttgagg 850  
gggtccccg ccttcacct ggctgtcatc gggtagggcg gggccgtggg 900  
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gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
cgtgggtgag tatgtgtgg gcacaggctg gctccctcag ctcacagtc 1100  
ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150  
gcggctgcag tccttttctc cctcaaaggt ctccgacct cagctggagg 1200  
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ccatggaggg gctgactgcc ccacattgcc ttccagacag gacacgagca 1350  
tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400  
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 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000  
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050  
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100  
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala	1	5	10	15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser	20	25	30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	35	40	45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	50	55	60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	65	70	75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	80	85	90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	95	100	105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	110	115	120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln				

	125		130		135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro					
	140		145		150

Ser Pro Arg Gly Asp Leu Pro  
155

<210> 357  
<211> 1536  
<212> DNA  
<213> Homo sapiens

<400> 357  
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cctcttatttt ctcttcacgt gtgagctggc tgcagaagtt gctgcagaag 100  
ttgagaaatc ctcatgtgtt cctgggtgtg cccaggaacc cacgtggctc 150  
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200  
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250  
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300  
gaggttctga cactactaaa catcactggg aacaccatct gcctctttcg 350  
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400  
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450  
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500  
tcagattcat ctctctctga taatgaacaa ggcctcccca gagtatgaag 550  
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600  
ctcttttattc tgggtggacag tggtagaaa gaaaatggga aggtgatatc 650  
atcttttcaaa cttaaaggagt ctcaactgcc agctttggca atttaccaga 700  
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750  
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800  
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850  
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900  
aactcaaate tcagagacac taaacaacag gatcactagg cctgccaaacc 950  
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000  
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050  
tctctttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100

cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150  
 tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200  
 ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
 cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300  
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
 tcaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400  
 cagaagttaa aggtgtgtct caagtcctg aactcagcag aaatagacca 1450  
 tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaatcaa 1500  
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
				20					25					30
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35					40					45
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50					55					60
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65					70					75
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80					85					90
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95					100					105
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110					115					120
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125					130					135
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140					145					150
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155					160					165



Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 359  
 ccagcagtgcc ccatactcca tagc 24

<210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 360  
 tgacgagtgg gatacactgc 20

<210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 361  
 gctctacgga aacttctgct gtgg 24

<210> 362  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
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ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagccaa 100  
cctcagcggg gaccggggct cagggacgcg gcggcggcgg cggcgactgc 150  
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200  
cccagacagc cggcgctggc tgtggtcggg gctggcgggc gcgcttgggc 250  
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300  
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tagtacgact ggcggttga cctcagtctc ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
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cctggacaca ttaggctcta tgctgtagaa aaagagaatt tgctgtgtt 650  
tccagtttgg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
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gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
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gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
 atgtagcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100  
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
 cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200  
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
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 ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400  
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 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccatttgg 1500  
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550  
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
 . tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700  
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
1				5					10					15
Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20					25					30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp  
 95 100 105  
 Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile  
 110 115 120  
 Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys  
 125 130 135  
 Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile  
 140 145 150  
 Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val  
 155 160 165  
 Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr  
 170 175 180  
 Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn  
 185 190 195  
 Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser  
 200 205 210  
 Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly  
 215 220 225  
 Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile  
 230 235 240  
 Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile  
 245 250 255  
 Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn  
 260 265

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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 ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150  
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200  
 aggggcgcgg ccccggcgca gtcccccgcg gccccgacc ctgaggcgtc 250  
 gcctctggcc gagecgccac aggagcagtc cctcgccccg tgggtctccgc 300  
 agacccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350  
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400

agtgggttga gtttctgtag atggaaaaga agtctgggtca gaagggttag 450  
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500  
 cgaattgcta gcatcagcaa aagtctcacc atgggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
 agattactga tttcccattt aagtggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
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 caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150  
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 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300  
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<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
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Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30

Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45

Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val  
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg  
365 370

<210> 367  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
tggaaaagaa gtctggtcag aaggtttagg 30

<210> 368  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 368  
catttgctt cattctctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 369  
aaaacctcag aacaactcat ttgcacc 28

<210> 370  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 370  
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<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
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 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
 tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
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 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

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Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30





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<210> 374  
 <211> 450  
 <212> PRT  
 <213> Homo sapiens

<400> 374  
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 35 40 45  
 Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala  
 50 55 60  
 Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly  
 65 70 75  
 Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu  
 80 85 90  
 Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys  
 95 100 105  
 Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu  
 110 115 120  
 Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala  
 125 130 135  
 Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala  
 140 145 150  
 Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu  
 155 160 165  
 Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val  
 170 175 180  
 Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp  
 185 190 195  
 Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu  
 200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn  
 215 220 225  
 Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu  
 230 235 240  
 Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile  
 245 250 255  
 Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp  
 260 265 270  
 Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe  
 275 280 285  
 Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg  
 290 295 300  
 Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu  
 305 310 315  
 Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr  
 320 325 330  
 Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile  
 335 340 345  
 Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser  
 350 355 360  
 Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala  
 365 370 375  
 Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys  
 380 385 390  
 Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr  
 395 400 405  
 Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu  
 410 415 420  
 Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu  
 425 430 435  
 Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu  
 440 445 450

<210> 375  
 <211> 1098  
 <212> DNA  
 <213> Homo sapiens

<400> 375  
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 gctccccgcg tgcgtcgcgg ccacagcgtt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgccaagg actttggtgg tatctttcac acaaggatatg agcagattca 250  
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 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650  
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750  
 tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800  
 cccagggccc ccaaggtgt ctcatgctac aagaagaggc aagagacagg 850  
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900  
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050  
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
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Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25						30

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40						45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr	50	55	60
Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly	65	70	75
Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val	80	85	90
Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln	95	100	105
Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp	110	115	120
Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg	125	130	135
Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr	140	145	150
Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile	155	160	165
Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu	170	175	180
Leu Gln Pro Pro Trp Thr Phe Trp	185		

<210> 377

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 396

<223> unknown base

<400> 377

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ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300
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tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
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Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25						30

Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45

Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60

Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75

Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90

His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105

Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu
			110						115	

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 381  
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<210> 382  
<211> 764  
<212> DNA  
<213> Homo sapiens

<400> 382  
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ctcctggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggtgtc 250  
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttga 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
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gcttctgcag aaaa 764

<210> 383  
<211> 178  
<212> PRT  
<213> Homo sapiens

<400> 383  
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1 5 10 15



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				20					25					30			
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr			
				35					40					45			
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln			
				50					55					60			
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly			
				65					70					75			
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr			
				80					85					90			
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met			
				95					100					105			
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly			
				110					115					120			
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val			
				125					130					135			
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly			
				140					145					150			
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro			
				155					160					165			
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg					
				170					175								

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

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ccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250

atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300

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 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000  
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<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

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Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala
				20					25					30
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val
				35					40					45
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser
				50					55					60
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys
				65					70					75
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu
				80					85					90
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe
				95					100					105
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg
				110					115					120
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu
				125					130					135
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser
				140					145					150

Glu Gln Phe Arg	Gly Leu Arg Lys Leu	Leu Ser Leu His Leu Arg
	155	160 165
Ser Asn Ser Leu	Arg Thr Ile Pro Val	Arg Ile Phe Gln Asp Cys
	170	175 180
Arg Asn Leu Glu	Leu Leu Asp Leu Gly	Tyr Asn Arg Ile Arg Ser
	185	190 195
Leu Ala Arg Asn	Val Phe Ala Gly Met	Ile Arg Leu Lys Glu Leu
	200	205 210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe
	215	220 225
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys
	230	235 240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu
	245	250 255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly
	260	265 270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu
	275	280 285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser
	290	295 300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu
	305	310 315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe
	320	325 330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu
	335	340 345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile
	350	355 360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu
	365	370 375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu
	380	385 390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly
	395	400 405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile
	410	415 420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu
	425	430 435

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys  
440 445 450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys  
455 460 465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr  
470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu  
485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttgggtgct 150  
ctcggacctta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200  
aacaccctaa tggctgggtat atctgggatcc tcctgctgct ggttttggtg 250  
gcagctcttc tctgtggagc tgtggctctc tgcctccagt gctggctgag 300  
gagaccccgga attgattctc acaggcgcac catggcagtt tttgctgttg 350  
gagacttgga ctctatttat gggacagaag cagctgtgag tccaactggt 400  
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450  
atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500  
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550  
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650  
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aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750  
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850  
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taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950  
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
gtctcagcaa aaacaagagg ttttatgcc caacctgaag aggaagaaat 1100  
tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
ccaacacggg gagaaaagaa aatttccct tttacagtaa tgaatgtggc 1200  
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250  
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
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<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
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Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp
			20						25					30
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln
			35						40					45
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu
			50						55					60
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys
			65						70					75
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala
			80						85					90
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala
			95						100					105
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro
			110						115					120
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser
			125						130					135
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr				
			140						145					

<210> 391

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

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<210> 392

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

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accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100

gacgcagctg acgcccgcctt attagctctc gctgcgctgc ccgggctcag 150

aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200

tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250

ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300

cttgctgaag atgaagaata tacaatattg aggataatatt tttctttttt 350

ttttcaagtc ttgatttggtg gcttacctca agttaccatt tttcagtcaa 400

gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450

tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatgtggg 500

gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550

gtcaagttac gtgagcaaact actagactta agcaaaagat atgttaaagc 600

tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650

tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700

atthttgcaac gattgggtgaa gctggagAAC aaagttgact atattgttgt 750

gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800

cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850

ttgaaaatca ccttggtgctg ctccatccac tgtggattat atcctatggc 900

agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950



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<211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 395

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Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20					25					30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35					40					45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50					55					60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65					70					75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80					85					90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95					100					105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110					115					120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125					130					135
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396

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 acctcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300  
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
 caccagcatc tcaccactg ccttctccc ccttcgctac ctggagtcgc 400

ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu
				20				25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys
				35				40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp
				50				55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn
				65				70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu
				80				85					90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe	Ser
95	100		105
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly	Leu
110	115		120
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser	Asp
125	130		135
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser	Ala
140	145		150
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp	Leu Ser
155	160		165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala	Gly
170	175		180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn	Arg
185	190		195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr	Leu
200	205		210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala	Phe
215	220		225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu	Gln
230	235		240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro	Gly
245	250		255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp	Ala
260	265		270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu	Asp
275	280		285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu	Leu
290	295		300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val	Arg
305	310		315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro	Gly
320	325		330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu	Ser
335	340		345
Ala Ala Arg Gly	Pro Thr Ile Leu		
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<210> 398  
 <211> 23  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

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<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

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<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

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atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

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 ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250  
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300  
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350  
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550  
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10				15	

Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20						25				30	

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35						40				45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	
				50					55					60	
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	
				65					70					75	
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	
				80					85					90	
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	
				95					100					105	
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	
				110					115					120	
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	
				125					130					135	
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	
				140					145					150	
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	
				155					160					165	
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	
				170					175					180	
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	
				185					190					195	
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	
				200					205					210	
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	
				215					220					225	
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	
				230					235					240	
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	
				245					250					255	
Trp	Met	Glu	Glu	Thr	Glu										
				260											

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgtggt ctccagattt caggccta 28



<210> 404  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50  
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactcaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgcctat ttacagacac gtagtgtatt ctggaggctc aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
tgcatTTgca aaaatccttag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tgggtgaatat gggagattta 650  
accacttatg atacagtga acactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtg agaatgaccc cttgggtcaat ggtgttctgg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln
1				5					10					15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
				80					85					90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95					100					105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110					115					120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
				125					130					135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
				140					145					150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
				155					160					165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
				170					175					180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
				185					190					195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr		
	260	265 270
Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly		
	275	280 285
Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met		
	290	295 300
Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg		
	305	310 315
Glu Met Ser Gly Val Ser Pro Phe		
	320	

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgcgatccc gttatcgtct tgcgtactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggaacgctg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150

tagataatth tcgttgcca gaatgtgaat gtattgactg gaggtagaga 200

agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtattht ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400  
 ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450  
 tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500  
 gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550  
 tgcacttata ttttttagca ctctgatcta caaatTTgga agaaccgaag 600  
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650  
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaTggag 700  
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750  
 ttgaaatagt tttatgaaat ttctttattt ttcatTgcat agactgttaa 800  
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850  
 tattctgag atttagaact tgatctactc cctgagccag ggTtacatca 900  
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950  
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000  
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100  
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150  
 aggttgcaTt gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200  
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250  
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300  
 cataaaaggT tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350  
 ttttttggtA aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400  
 tttatataat gatTTTTtaa atgcccaaag gactagtttg aaagcttctt 1450  
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
1				5					10				15	

Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 411  
 gtttgaggaa gctgggatac 20

<210> 412  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 412  
 ccaaactcga gcacctgttc 20

<210> 413  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 413

atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 414

gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50

gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100

actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200

gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250

aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300

acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcctc 350

tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400

catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450

agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500

aactactttg cgtttaaaat ctgcagtggg gccgccaaag tcgtgggccc 550

tactatgtgc tttgaagacc gcatgatcat gagtctctgtg aaaaacaatg 600

tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650

ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700

gaaattcctt aaagaaatc cggggggtgc actggtgctg gtggcctcct 750

acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800

gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850

cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900

taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950

gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000

ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050

cccggcaggg gctgaggagg aggagcaggg ggtgctgctg ggaagggtgct 1100

gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaacct 1150

tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200

accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250  
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300  
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415

<211> 224

<212> PRT

<213> Homo sapiens

<400> 415

Met	Arg	Val	Ser	Gly	Val	Leu	Arg	Leu	Leu	Ala	Leu	Ile	Phe	Ala	1	5	10	15
Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

<210> 416  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 416  
gccatagtca cgacatggat g 21

<210> 417  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 417  
ggatggccag agctgctg 18

<210> 418  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 418  
aaagtacaag tgtggcctca tcaagc 26

<210> 419  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 419  
tctgactcct aagtcaggca ggag 24

<210> 420  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 420  
attctctcca cagacagctg gttc 24

<210> 421



<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 421  
gtacaagtgt ggccatcatca agccctgccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgctcgc tctctctctc tctctctcac tctccctcc 200  
ctctctctct gcctgtccta gtccctctagt cctcaaattc ccagtccct 250  
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggaggtg 300  
atttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350  
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtgc actctctctg cctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600  
cactgggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850  
ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900

cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950  
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000  
 ttcagggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050  
 cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100  
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
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 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300  
 catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350  
 ggggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400  
 cttccccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450  
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
 gaaatcgctg tgttgttaat gcagaganca aactctgttt agttgcaggg 1550  
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600  
 tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650  
 gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700  
 t 1701

<210> 423  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 423  
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
   1                  5                  10                  15  
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
                   20                  25                  30  
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
                   35                  40                  45  
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
                   50                  55                  60  
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
                   65                  70                  75  
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu  
                   80                  85                  90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala
95	100 105
Ala Gln Leu His Leu His Trp Gly Gln	Lys Gly Ser Pro Gly Gly
110	115 120
Ser Glu His Gln Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu His
125	130 135
Ile Val His Tyr Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu Ala
140	145 150
Ala Glu Arg Pro Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile Glu
155	160 165
Val Gly Glu Thr Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser His
170	175 180
Leu His Glu Val Arg His Lys Asp Gln	Lys Thr Ser Val Pro Pro
185	190 195
Phe Asn Leu Arg Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr Phe
200	205 210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val
215	220 225
Leu Trp Thr Val Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu Gln
230	235 240
Leu Glu Lys Leu Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu Pro
245	250 255
Ser Lys Leu Leu Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu Asn
260	265 270
Gln Arg Met Val Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser Tyr
275	280 285
Thr Thr Gly Glu Met Leu Ser Leu Gly	Val Gly Ile Leu Val Gly
290	295 300
Cys Leu Cys Leu Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys Ile
305	310 315
Arg Lys Lys Arg Leu Glu Asn Arg Lys	Ser Val Val Phe Thr Ser
320	325 330
Ala Gln Ala Thr Thr Glu Ala	
335	

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<211> 18

<212> DNA

<213> Artificial Sequence

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 <400> 425  
 cccgatctgc ctgctgta 18  
  
 <210> 426  
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 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45  
  
 <210> 428  
 <211> 1073  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 428  
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 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
  
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150  
  
 aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaca 200  
  
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300

ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350  
 ggggtgaatg tacaacagca actgcacca catgtgttac caatttttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gaggctcatc atccattcct tgttcccggg aggcatacctg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600  
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccacccct 650  
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700  
 agcaaattga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750  
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30

Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45

Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50						55					60

Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65						70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
			80						85					90

Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95		100		105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu	Ser Ser Glu Glu Leu	Pro		
	110		115		120
Gln Ile Phe Thr	Ser Leu Ile Ile His	Ser Leu Phe Pro Gly	Gly		
	125		130		135
Ile Leu Pro Thr	Ser Gln Ala Gly Ala	Asn Pro Asp Val Gln	Asp		
	140		145		150
Gly Ser Leu Pro	Ala Gly Gly Ala Gly	Val Asn Pro Ala Thr	Gln		
	155		160		165
Gly Thr Pro Ala	Gly Arg Leu Pro Thr	Pro Ser Gly Thr Asp	Asp		
	170		175		180
Asp Phe Ala Val	Thr Thr Pro Ala Gly	Ile Gln Arg Ser Thr	His		
	185		190		195
Ala Ile Glu Glu	Ala Thr Thr Glu Ser	Ala Asn Gly Ile Gln			
	200		205		

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 ccgcctccag ctccgcgctg ccgggcagcc gggagccatg cgaccccagg 150  
 gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200  
 ctgcagctgc ccgcgccgtc gagcgccctct gagatcccca aggggaagca 250  
 aaaggcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300  
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350  
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400  
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450  
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500  
 aaaattgagg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600  
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650  
 attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700

aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750  
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
ttattatgcc ttggaatggt tcacttaaata gacattttta ataagtttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagt 1000  
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100  
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
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tccaaca 1257

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<400> 431

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Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
230 235 240

Leu Pro Lys

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<213> Artificial Sequence

<220>

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<400> 432

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<210> 433

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<400> 433

cgcaggacag ttgtgaaaat a 21

<210> 434

<211> 21

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<400> 434

atgacgctcg tccaaggcca c 21



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cccacctgta ccaccatgt 19  
  
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<213> Artificial Sequence  
  
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<400> 436  
actccaggca ccatctgttc tccc 24  
  
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tgacctggca aaggaagaa 19  
  
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tcctccatca cttcccctag ctcca 25

<210> 443  
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<210> 444  
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<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
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<400> 445  
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<210> 446  
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<210> 447  
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<400> 450

ccctagctga ccccttca 18

<210> 451

<211> 23

<212> DNA

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<210> 452

<211> 26

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<210> 454

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 454

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<210> 455

<211> 23

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<223> Synthetic oligonucleotide probe

<400> 455  
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<210> 456  
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<400> 456  
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<210> 457  
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<210> 460  
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<210> 467  
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<210> 471  
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<400> 471  
cgagtgtgtg cgaaacctaa 20

<210> 472  
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<220>

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<210> 473  
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<210> 476  
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<400> 476

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<210> 477

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<212> DNA

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